

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 6, 2005, 19:40:10 ; Search time 191 Seconds
(without alignments)
1042.302 Million cell updates/sec

Title: US-10-041-859-2
Perfect score: 1887
Sequence: 1 MELTKVAKNGAATLVMLKN.....TDKCPMCRTFTNAVRLYFS 346

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1887	100.0	346	2 Q968T8	Q968T8 bombyx mori
2	1866	98.9	346	2 Q8IS31	Q8IS31 bombyx mori
3	1327	70.3	379	2 Q9U492	Q9U492 trichoplusi
4	1311	69.5	377	2 Q9NJ07	Q9NJ07 epodoptera
5	966	51.2	275	1 IAP GVCP	P41436 cydia pomon
6	937	49.7	287	2 Q6E7G7	Q6E7G7 anticarsia
7	890.5	47.2	280	2 Q6VTV9	Q6VTV9 choristoneu
8	890.5	47.2	280	2 AAQ91688	AAQ91688 choristoneu
9	879	46.6	263	2 Q80SF4	Q80SF4 hyphantria
10	876	46.4	281	2 Q9YNL8	Q9YNL8 choristoneu
11	873	46.3	261	2 Q9QES9	Q9QES9 epiphyas po
12	873	46.3	276	2 Q89744	Q89744 buzura sup
13	862	45.7	268	1 IAP3 NPVOP	P41437 oxygia pseu
14	782	41.4	264	2 Q9EN27	Q9EN27 amasacta moo
15	747.5	39.6	255	2 Q7T5S1	Q7T5S1 ctyptophleb
16	728	38.6	289	2 Q7QJ55	Q7QJ55 anopheles g
17	728	38.6	313	2 Q9J827	Q9J827 epodoptera
18	723.5	38.3	438	1 IAP1 DROME	Q24306 drosophila
19	719.5	38.1	438	2 Q9VUX5	Q9VUX5 drosophila
20	701	37.1	403	2 Q8WRD9	Q8WRD9 aedes tribe
21	684	36.2	401	2 Q6Q507	Q6Q507 aedes aegyp
22	684	36.2	401	2 AAS66751	AAS66751 aedes aeg
23	676.5	35.9	402	2 Q8T621	Q8T621 aedes albop
24	662	35.1	285	2 Q8JML6	Q8JML6 mamestra co
25	653	34.6	276	2 Q7IA73	Q7IA73 mamestra co
26	653	34.6	276	2 Q8QL95	Q8QL95 mamestra co
27	653	34.6	276	2 AAQ11158	AAQ11158 mamestra
28	635	33.7	283	2 Q8OLK8	Q8OLK8 adoxophyes
29	573	30.4	254	2 Q7T9S6	Q7T9S6 adoxophyes
30	544.5	28.9	269	2 Q6QXJ6	Q6QXJ6 agrotis seg
31	544.5	28.9	269	2 AAS82685	AAS82685 agrotis s

32	542	28.7	358	1 P1AP PIG	Q62640 sus scrofa
33	532.5	28.2	268	2 Q9E232	Q9E232 helicoverpa
34	530.5	28.1	401	2 Q8JHV9	Q8JHV9 xenopus lae
35	529.5	28.1	268	2 Q77LW6	Q77LW6 helicoverpa
36	529.5	28.1	268	2 Q9IF18	Q9IF18 helicoverpa
37	528.5	28.0	602	2 Q9ESE9	Q9ESE9 rattus norv
38	526.5	27.9	604	1 BIR3 HUMAN	Q13489 homo sapien
39	525.5	27.8	600	1 BIR3 MOUSE	Q08863 mus musculu
40	520.5	27.6	604	2 Q6DDY3	Q6DDY3 xenopus lae
41	516.5	27.4	616	2 Q804E2	Q804E2 ictalurus p
42	513.5	27.2	604	2 Q6GLD7	Q6GLD7 xenopus tro
43	513	27.2	628	2 Q8UWD2	Q8UWD2 brachydanio
44	513	27.2	647	2 Q7T0K2	Q7T0K2 brachydanio
45	513	27.2	654	2 Q6ZM93	Q6ZM93 brachydanio

ALIGNMENTS

RESULT 1	ID	Q968T8	PRELIMINARY;	PRT;	346 AA.
AC	Q968T8;	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)				
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)				
DE	Inhibitor of apoptosis protein.				
GN	Name=IAP;				
OS	Bombyx mori (Silk moth).				
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;				
OC	Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;				
OC	Bombycidae; Bombyx.				
OX	NCBI_TaxID=7091;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=21240184; PubMed=11341966;				
RA	Huang Q., Deveraux Q.L., Maeda S., Stennicke H.R., Hammock B.D.,				
RA	Reed J.C.;				
RT	"Cloning and characterization of an inhibitor of apoptosis protein				
RT	(IAP) from Bombyx mori."				
RL	Biochim. Biophys. Acta 1499:191-198(2001).				
DR	EMBL; AF281073; AAK57560.1; --				
DR	HSSP; Q24306; 1JD4.				
DR	GO; GO:0000151; C:ubiquitin ligase complex; IEA.				
DR	GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.				
DR	GO; GO:0008270; F:zinc ion binding; IEA.				
DR	GO; GO:0006916; P:anti-apoptosis; IEA.				
DR	GO; GO:0016567; P:protein ubiquitination; IEA.				
DR	InterPro; IPR001370; BIR.				
DR	InterPro; IPR001841; Znf_ring.				
DR	Pfam; PF00653; BIR; 2.				
DR	SMART; SM00238; BIR; 2.				
DR	SMART; SM00184; RING; 1.				
DR	PROSITE; PS01282; BIR_REPEAT_1; 2.				
DR	PROSITE; PS0143; BIR_REPEAT_2; 2.				
DR	PROSITE; PS50089; ZF_RING_2; 1.				
DR	SEQUENCE 346 AA; 38942 MW; 6CFC6C6468894C69 CRC64;				
QY	Query Match	100.0%;	Score 1887;	DB 2;	Length 346;
QY	Best Local Similarity	100.0%;	Pred. No. 1e-149;		
QY	Matches 346;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1 MELTKVAKNGAATLVMLKNARDAKMRPFIGPLMLSGCESSSTSTLPSSSSADKTDNHD 60				
Db	1 MELTKVAKNGAATLVMLKNARDAKMRPFIGPLMLSSCESSSTSTLPSSSSADKTDNHD 60				
QY	61 TFNPLPDMPMRREBERLKTFDQWPVTLTPEQLARNGFYLLGRGDEVCCAFCKVEIMRW 120				
Db	61 TFNPLPDMPMRREBERLKTFDQWPVTLTPEQLARNGFYLLGRGDEVCCAFCKVEIMRW 120				
QY	121 VEGDDPADHRRWAPQCPFRKQMYANAGGEATAVGRDECGASATQPRMPGVHARYS 180				
Db	121 VEGDDPADHRRWAPQCPFRKQMYANAGGEATAVGRDECGASATQPRMPGVHARYS 180				

QY 181 TEAARLATFKDWMRRMRQKPEELAEAGFFYTGQDKTKCFYCDGGLKDWESDVPWEQHA 240
Db 181 TEAARLATFKDWMRRMRQKPEELAEAGFFYTGQDKTKCFYCDGGLKDWESDVPWEQHA 240
QY 241 RWFDRCAVYQLVKGRDYIQVKSEATAISASEEQAAATNDSTKNVAQEGEKHLDSKICK 300
Db 241 RWFDRCAVYQLVKGRDYIQVKSEATAISASEEQAAATNDSTKNVAQEGEKHLDSKICK 300
QY 301 ICYSEERNVCFVPCGHVAVACAKCALSTDKCPMCRRTFTNAVRLYFS 346
Db 301 ICYSEERNVCFVPCGHVAVACAKCALSTDKCPMCRRTFTNAVRLYFS 346

RESULT 2
Q8IS31 PRELIMINARY; PRT; 346 AA.
ID Q8IS31;
AC Q8IS31;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)
DE Inhibitor of apoptosis protein.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang G., Wang L., Wu X.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY155274; AAN46650.1; -.
DR HSSP; Q24306; 1JD4.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00238; BIR; 2.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 2.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 346 AA; 38849 MW; 5450EB75F56A8486 CRC64;

Query Match 98.9%; Score 1866; DB 2; Length 346;
Best Local Similarity 99.1%; Pred. No. 6e-148;
Matches 343; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MELTKVAKNGAATLVMLKNARDAKMRPFIPLMLSSCESSTSTLPSSSADKTNDHD 60
Db 1 MELTKVAKNGAATLVMLKNARDAKMRPFIPLMLSSCESSTSTLPSSSADKTNDHD 60
QY 61 TTNFLPDMPMRREERLKTFFDQWVPTFTLTPQOLARNGFYILGRGDEVCCAFCKVEIMRW 120
Db 61 TTNFLPDMPMRREERLKTFFDQWVPTFTLTPQOLARNGFYILGRGDEVCCAFCKVEIMRW 120
QY 121 VEGDDPADHRRWAPQCPFVRKQMYANAGGEATAVGRDECGASATQPPRMPGVHARYS 180
Db 121 VEGDDPADHRRWAPQCPFVRKQMYANAGGEAAVGRDECGASATQPSRMPGVHARYS 180
QY 181 TEAARLATFKDWMRRMRQKPEELAEAGFFYTGQDKTKCFYCDGGLKDWESDVPWEQHA 240
Db 181 TEAARLATFKDWMRRMRQKPEELAEAGFFYTGQDKTKCFYCDGGLKDWESDVPWEQHA 240
QY 241 RWFDRCAVYQLVKGRDYIQVKSEATAISASEEQAAATNDSTKNVAQEGEKHLDSKICK 300
Db 241 RWFDRCAVYQLVKGRDYIQVKSEATAISASEEQAAATNDSTKNVAQEGEKHLDSKICK 300
QY 301 ICYSEERNVCFVPCGHVAVACAKCALSTDKCPMCRRTFTNAVRLYFS 346

Db 301 ICYSEERNVCFVPCGHVAVACAKCALSTDKCPMCRRTFTNAVRLYFS 346

RESULT 3
Q9U492 PRELIMINARY; PRT; 379 AA.
ID Q9U492;
AC Q9U492;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, last annotation update)
DE Inhibitor of apoptosis protein.
GN Name=IAP1;
OS Trichoplusia ni (Cabbage looper).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Plusiinae; Trichoplusia.
OX NCBI_TaxID=7111;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20062908; PubMed=10593985;
RA Seshagiri S., Vucic D., Lee J., Dixit V.M.;
RT "Baculovirus-based genetic screen for antiapoptotic genes identifies a novel IAP."
RL J. Biol. Chem. 274:36769-36773(1999).
DR EMBL; AF195528; AAF19819.1; -.
DR HSSP; Q24306; 1JD4.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00238; BIR; 2.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 2.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 379 AA; 41857 MW; 069381A012D9DE65 CRC64;

Query Match 70.3%; Score 1327; DB 2; Length 379;
Best Local Similarity 69.0%; Pred. No. 9.8e-103;
Matches 251; Conservative 39; Mismatches 54; Indels 20; Gaps 8;
QY 1 MELTKVAKNGAATLVMLKNA-RDAKMRPFIPLML--SSCESSTSTLPSPS----- 51
Db 18 MDITKVASNGPASPLTLFKNAPRDAKIRPLV-PLVLPQTQSYDSNAGSPASSPTSSSSS 76
QY 52 -SADKTDNHTFNFLPDMPMRREERLKTFFDQWVPTFTLTPQOLARNGFYILGRGDEVCC 110
Db 77 FSIDKTDNHTFSLTADAVDMSREDERIKTFEKWPEVSFLSGEQLARNGFYILGRGDEVRC 136
QY 111 AFCKVEIMRWVEGDDPADHRRWAPQCPFVRKQMYANAGGEATAVGRDECGASAA--TOP 168
Db 137 AFCKVEIMRWVEGDDPAKDHRWAPQCPFVRK-LGGGVNTDSGAAGRDECGARAAPTSSP 195
QY 169 PRMPGVHARYSTEARLATFKDWMRRMRQKPEELAEAGFFYTGQDKTKCFYCDGGLKD 228
Db 196 SRMPGVHPRYASEARLRSFKDWMRRMRQKPEELAEAGFFYTGQDKTKCFYCDGGLKD 255
QY 229 WESDDVPWEQHARWFDRCAYVQLVKGRDYIQVKSEATAI---SASEE---QAATNDST 282
Db 256 WENDDVPWEQHARWFDRCAYVQLVKGREYQKVMTEACVIPAAPRDEAPARSAAEPSV 315
QY 283 KNVAQEGEKHLDSKICKICYSEERNVCFVPCGHVAVACAKCALSTDKCPMCRRTFTNAV 342
Db 316 VSAEPQESTLDSKICKICFAEERNVCFVPCGHVAVACAKCALAADKCPMCRRTFTQNAVR 375
QY 343 LYFS 346
Db 376 LYFS 379

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 13, 2005, 13:40:00 ; Search time 6731 Seconds
(without alignments)
1873.146 Million cell updates/sec

Title: US-10-041-859-2

Perfect score: 1887

Sequence: 1 MELTKVAKNGAATLVMLKN.....TDKCPMCRTFTNAVRLYFS 346

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2.1/USPTO_spool/US10041859/runat_10012005_155634_27790/app_query.fasta_1.519
-DB=EST -QFMT=fastcap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pcio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10041859_QCGN_1_1_3437@runat_10012005_155634_27790 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOC
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gss1: *
9: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1053	55.8	712	5 BP121000	BP121000 BP121000
2	1053	55.8	727	5 BP120885	BP120885 BP120885
3	985	52.2	723	1 AV401669	AV401669 AV401669
4	928	49.2	622	7 CK497882	CK497882 rswb0_00
5	861.5	45.7	555	5 BP121882	BP121882 BP121882
6	812	43.0	512	1 AV398511	AV398511 AV398511
7	684	36.2	500	5 BP115618	BP115618 BP115618
8	647	34.3	804	9 CG786123	CG786123 CM_MBA-76
9	545	28.9	1288	3 CR688416	CR688416 Tetraodon

10	536	28.4	1353	3 CR692095	CR692095 Tetraodon
11	520	27.6	1347	3 CR729221	CR729221 Tetraodon
12	519	27.5	522	7 CK516014	CK516014 rawjb0_00
13	514	27.2	723	7 CO640316	CO640316 USDA-FP_1
14	510.5	27.1	1778	9 AY420755	AY420755 Mus muscu
15	503	26.7	2079	3 CR733861	CR733861 Tetraodon
16	500.5	26.5	782	6 CB690915	CB690915 Cy23 Aede
17	498.5	26.4	712	4 BM601939	BM601939 170006870
18	497	26.3	1439	3 CR702049	CR702049 Tetraodon
19	493.5	26.2	1799	9 AY420753	AY420753 Homo sapi
20	488	25.9	2047	3 CR724410	CR724410 Tetraodon
21	486	25.8	1851	3 BC056914	BC056914 Homo sapi
22	484	25.6	1789	3 BC046168	BC046168 Homo sapi
23	467	24.7	864	7 CK189215	CK189215 EST778530
24	453.5	24.0	718	3 AY432429	AY432429 Aedes aeg
25	446.5	23.7	887	7 CN502150	CN502150 AGENCOURT
26	446	23.6	771	6 CA803224	CA803224 ESG011a.B
27	445	23.6	727	7 CF525095	CF525095 AGENCOURT
28	445	23.6	1045	7 CN645252	CN645252 ILLUMIGEN
29	440.5	23.3	881	6 CF265917	CF265917 AGENCOURT
30	437	23.2	950	7 CO647969	CO647969 ILLUMIGEN
31	435	23.1	886	5 BQ652590	BQ652590 AGENCOURT
32	428	22.7	567	4 BI961039	BI961039 MONOI_5_C
33	426.5	22.6	678	6 CA805412	CA805412 ESG0118a.
34	426.5	22.6	910	6 CA981958	CA981958 AGENCOURT
35	425.5	22.5	745	7 CN062644	CN062644 Ag2_p37_J
36	425	22.5	887	4 BJ728878	BJ728878 BJ728878
37	423	22.4	937	6 CA981608	CA981608 AGENCOURT
38	421.5	22.3	781	6 CF152602	CF152602 AGENCOURT
39	421	22.3	1084	5 BU902159	BU902159 AGENCOURT
40	420	22.3	644	1 AL854961	AL854961 AGENCOURT
41	418.5	22.2	929	6 CA981777	CA981777 AGENCOURT
42	415	22.0	586	7 CF913919	CF913919 B0956C11-
43	414.5	22.0	857	6 CA985214	CA985214 AGENCOURT
44	414	21.9	851	4 BI253303	BI253303 602973538
45	413.5	21.9	909	6 CA981433	CA981433 AGENCOURT

ALIGNMENTS

RESULT 1
BP121000 LOCUS BP121000 712 bp mRNA linear EST 16-MAY-2003
DEFINITION BP121000 cen- Bombyx mori cDNA clone cen-4016, mRNA sequence.
ACCESSION BP121000
VERSION BP121000.1 GI:29554042
KEYWORDS EST.
SOURCE Bombyx mori (domestic silkworm)
ORGANISM Bombyx mori

REFERENCE
AUTHORS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
TITLE Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
JOURNAL Bombycidae; Bombycidae; Bombyx.
COMMENT 1 (bases 1 to 712)
Mita,K., Morimyo,M., Shimada,T., Okano,K. and Maeda,S.
Bombyx mori cDNA (Mita,K. 2003)
Unpublished (2003)
Contact: Mita K
Genome Research Group
National Institute of Agrobiological Sciences
Owashi 1-2, Tsukuba, Ibaraki 305-8634, Japan
Email: kmita@nias.affrc.go.jp
method:uni-directional, sequence direction:sequenced from T3 primer
(5' -> 3').

FEATURES

source
1..712
/organism="Bombyx mori"
/mol_type="mRNA"
/db_xref="taxon:7091"
/clone="cen-4016"
/tissue_type="compound eye"
/clone_lib="cen-"
/note="Mixed stages from 5th instar larva to pupa"

ORIGIN

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 6, 2005, 19:48:11 ; Search time 40 Seconds
(without alignments)
832.275 Million cell updates/sec

Title: US-10-041-859-2

Perfect score: 1887

Sequence: 1 MELTKVAKNGAATLVMLKN.....TDKCPMCRRFTNAVRLYFS 346

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB	ID	Description
1	966	51.2	275	2	A45679	inhibitor-of-apopt
2	862	45.7	268	2	T10304	inhibitor of apopt
3	862	45.7	268	2	A53989	apoptosis-inhibiti
4	542	28.7	358	2	JCS964	apoptosis inhibito
5	524.5	27.8	604	2	S68449	apoptosis inhibito
6	507.5	26.9	618	2	S68450	apoptosis inhibito
7	501	26.6	497	2	S69545	apoptosis inhibito
8	500.5	26.5	496	2	S68452	apoptosis inhibito
9	497.5	26.4	497	2	S69544	apoptosis inhibito
10	381.5	20.2	292	2	T41772	apoptosis inhibito
11	378	20.0	286	2	D36828	API orf27 - Bomby
12	369.5	19.6	275	2	T10310	orf13 protein - Au
13	362.5	19.2	298	2	JC7568	apoptosis-inhibiti
14	309	16.4	1447	2	T42628	kidney inhibitor o
15	299	15.8	1232	2	A55478	neuronal apoptosis
16	253	13.4	208	2	T03183	probable apoptosis
17	252.5	13.4	150	2	T28409	ORF MSV248 probabl
18	232	12.3	234	2	T30427	probable apoptosis
19	222.5	11.8	155	2	T30489	apoptosis inhibito
20	220.5	11.7	997	2	T43523	cutl7 protein - fi
21	171.5	9.1	308	2	T37474	apoptosis inhibito
22	164.5	8.7	249	2	T41814	IAP2 orf71 - Bomby
23	164.5	8.7	329	2	T28403	ORF MSV242 probabl
24	159.5	8.5	249	2	H72858	apoptosis inhibito
25	156	8.3	236	2	T10343	inhibitor of apopt
26	155.5	8.2	383	2	F96582	hypothetical prote
27	154	8.2	4845	2	T31067	BIR repeat contain
28	149.5	7.9	115	2	B96664	probable RING zinc
29	139	7.4	124	2	T01251	hypothetical prote

30	132.5	7.0	864	2	T01393	apoptosis inhibito
31	131.5	7.0	489	2	S15349	mdm2 protein - mou
32	130	6.9	428	2	T48167	hypothetical prote
33	122.5	6.5	237	2	T52432	hypothetical prote
34	122.5	6.5	823	2	D86165	protein F15K9.3 [i
35	120	6.4	711	2	C84767	hypothetical prote
36	120	6.4	943	2	S68824	rn8B protein, cyto
37	119	6.3	433	2	JC7678	RING finger protei
38	117	6.2	491	1	S24354	p53-binding protei
39	116	6.1	754	2	S35503	finger protein neu
40	115	6.1	401	2	G96824	hypothetical prote
41	115	6.1	529	2	T19204	hypothetical prote
42	114	6.0	337	2	T48341	hypothetical prote
43	114	6.0	372	2	C96631	hypothetical prote
44	113.5	6.0	269	2	T40371	probable zinc fing
45	112	5.9	204	2	T01447	hypothetical prote

ALIGNMENTS

RESULT 1

A45679

inhibitor-of-apoptosis polypeptide (IAP) - Cydia pomonella granulosis virus CpgV

C/Species: Cydia pomonella granulosis virus CpgV

C/Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C/Accession: A45679

R/Crook, N.E.; Clem, R.J.; Miller, L.K.

J. Virol. 67, 2168-2174, 1993

A/Title: An apoptosis-inhibiting baculovirus gene with a zinc finger-like motif.

A/Reference number: A45679; MWID:93188168; PMID:8445726

A/Accession: A45679

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-275 <CRO>

A/Cross-references: UNIPROT:P41436; GB:L05494; NID:G289583; PIDN:AAA3835.1; PID:G28958

A/Note: sequence extracted from NCBI backbone (NCBIIN:127014, NCBIIP:127015)

C/Superfamily: viral apoptosis inhibitor IAP; RING finger homology

Query Match

Best Local Similarity 51.2%; Score 966; DB 2; Length 275;

Matches 171; Conservative 39; Mismatches 55; Indels 24; Gaps 3;

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DB	61	ADHKWAPQCPFKV-----GIDVCGSIYTTNNIQNTTHTDTITGPAHPKYA	106
QY	181	TEARLATFKDWRPRMRQKPEELAEAGFFYTGQDKTKCFYCDGGLKDWESDVPWEQHA	240
DB	107	HEARVKSFHNPWRCMKQPEQADAGFFYTGYNKCFYCDGGLKDWEPEDVPWEQHV	166
QY	241	RWFDRCAYVOLVKGRDYIQVKSEATAI---SASEEQATNDSTKNVAQEGEKHLDISK	297
DB	167	RWFDRCAYVOLVKGRDYQKVTTEACVLPGENTTVSTAPVSEPIPETKIEKEPVEDSK	226
QY	298	ICKICYSEBRNVCFVPCGVAVACAKCALSTDKCPMCRRFTNAVRLYFS	346
DB	227	LCKICYBECIVCFVPCGVAVACAKCALSDVKCPMCKRITSVLKVYFS	275

RESULT 2

T10304

inhibitor of apoptosis protein 3 - Orgyia pseudotsugata nuclear polyhedrosis virus

C/Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OpMNPV

C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Sep-2000

C/Accession: T10304

R/Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F.

Virolology 229, 381-399, 1997

A/Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosi

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 13, 2005, 15:56:25 ; Search time 650 Seconds
(without alignments)
3058.581 Million cell updates/sec

Title: US-10-041-859-2
Perfect score: 1887
Sequence: 1 MELTKVAKXNGAALTVMLKN.....TDKCPMCRRFTNAVRLYFS 346

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=b1ts -START=1 -END=-1 -MATRIX=blosum62
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Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Length	DB ID	Description
1	1887	100.0	3773	14 US-10-041-859-1	Sequence 1, Appli
2	719.5	38.1	1317	16 US-10-267-502-202	Sequence 202, App
3	526.5	27.9	2563	16 US-10-305-720-1076	Sequence 1076, App
4	526.5	27.9	2563	16 US-10-641-643-894	Sequence 894, App
5	526.5	27.9	2601	15 US-10-232-286-3	Sequence 3, Appli
6	526.5	27.9	3076	9 US-09-954-456-1635	Sequence 1635, Ap
7	526.5	27.9	3076	9 US-09-954-531-16	Sequence 16, Appli
8	526.5	27.9	3076	14 US-10-197-290-1	Sequence 1, Appli
9	526.5	27.9	3076	15 US-10-388-263-157	Sequence 157, App
10	526.5	27.9	3076	17 US-10-776-827-11	Sequence 11, Appli
11	526.5	27.9	3165	15 US-10-141-618-5	Sequence 5, Appli
12	526.5	27.9	3165	15 US-10-269-909-5	Sequence 5, Appli
13	526.5	27.9	3165	15 US-10-172-118-564	Sequence 564, App
14	526.5	27.9	3165	15 US-10-366-307-5	Sequence 5, Appli
15	526.5	27.9	3165	16 US-10-342-887-564	Sequence 564, App
16	526.5	27.9	5212	18 US-10-825-282-39	Sequence 39, Appli
17	526.5	27.9	5844	10 US-09-971-392-253	Sequence 253, App
18	526.5	27.9	5857	15 US-10-247-671-18	Sequence 18, Appli
19	525.5	27.8	2673	18 US-10-482-952-2	Sequence 2, Appli
20	525.5	27.8	2676	9 US-09-974-592-11	Sequence 11, Appli
21	525.5	27.8	6669	9 US-09-974-592-5	Sequence 5, Appli
22	525.5	27.8	6669	17 US-10-636-065-230	Sequence 230, App
23	524.5	27.8	2676	9 US-09-201-936-5	Sequence 5, Appli
24	524.5	27.8	2676	17 US-10-636-065-220	Sequence 220, App
25	524.5	27.8	2676	17 US-10-600-272-5	Sequence 5, Appli
26	524.5	27.8	2916	16 US-10-240-425-1436	Sequence 1436, Ap
27	524.5	27.8	2916	17 US-10-776-827-31	Sequence 31, Appli
28	517.5	27.4	2450	9 US-09-201-936-39	Sequence 39, Appli
29	517.5	27.4	2474	17 US-10-636-065-226	Sequence 226, App
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31	514.5	27.3	3153	18 US-10-482-952-10	Sequence 10, Appli
32	507.5	26.9	2580	9 US-09-201-936-7	Sequence 7, Appli
33	507.5	26.9	2580	17 US-10-636-065-222	Sequence 222, App
34	507.5	26.9	2580	17 US-10-600-272-7	Sequence 7, Appli
35	500.5	26.5	2531	15 US-10-207-655-199	Sequence 199, App
36	500.5	26.5	2589	15 US-10-232-286-1	Sequence 1, Appli
37	500.5	26.5	2589	17 US-10-730-476A-42	Sequence 42, Appli
38	500.5	26.5	2589	17 US-10-730-476A-43	Sequence 43, Appli
39	500.5	26.5	3495	18 US-10-482-952-12	Sequence 12, Appli
40	500.5	26.5	3496	14 US-10-153-668-337	Sequence 337, App
41	500.5	26.5	3496	15 US-10-172-118-565	Sequence 565, App
42	500.5	26.5	3496	15 US-10-366-307-3	Sequence 3, Appli
43	500.5	26.5	3496	16 US-10-342-887-565	Sequence 565, App
44	500.5	26.5	3496	16 US-10-260-708-18	Sequence 18, Appli
45	500.5	26.5	3532	9 US-09-880-107-3354	Sequence 3354, Ap

ALIGNMENTS

RESULT 1
US-10-041-859-1
; Sequence 1, Application US/10041859
; Publication No. US20030049796A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, QIHONG
; APPLICANT: REED, JOHN C.
; APPLICANT: DEVERAUX, QUINN L.
; APPLICANT: MAEDA, SUSUMU
; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND
; TITLE OF INVENTION: METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 087102/027 2537
; CURRENT APPLICATION NUMBER: US/10/041, 859
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260, 478
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3773
; TYPE: DNA

ORGANISM: Bombyx mori
FEATURE:
NAME/KEY: CDS
LOCATION: (2733)..(3770)
US-10-041-859-1

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US-10-041-859-2 (1-346) x US-10-041-859-1 (1-3773)

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QY      21 AlaArgAspAlaLysMetArgProPheIleGlyProLeuMetLeuSerSerCysGluSer 40
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QY      41 SerThrThrSerThrLeuProSerProSerSerSerAlaAspLysThrAspAsnHisAsp 60
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QY      61 ThrPheAsnPhelLeuProAspMetProAspMetArgArgGluGluGluArgLeuLysThr 80
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QY      81 PheAspGlnTrpProValThrPheLeuThrProGluGlnLeuAlaArgAsnGlyPheTyr 100
DB      446 TTTGATCAGTGCGCCGTTACGTTTGTGACGCCCGGAACAATTGGCCCGCAACGGAATCTAC 505
QY      101 TyrLeuGlyArgGlyAspGluValCysCysAlaPheCysLysValGluLeuMetArgTrp 120
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QY      141 ArgLysGlnMetTyrAlaAsnAlaGlyGlyGluAlaThrAlaValGlyArgAspGluCys 160
DB      626 CGAAAACAAAATGATGCCAACGCTGGGGGAGGCGACCGCTGCGGTAGAGACGAATGT 685
QY      161 GlyAlaSerAlaAlaThrGlnProProArgMetProGlyProValHisAlaArgTyrSer 180
DB      686 GGGGCCAGTGGCGCCACGACGCTCCCGCATGCCCCGCGCCCGTGCACGCGCGGTACTCC 745
QY      181 ThrGluAlaAlaArgLeuAlaThrPheLysAspTrpProArgArgMetArgGlnLysPro 200
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QY      201 GluGluLeuAlaGluAlaGlyPhePheTyrThrGlyGlnGlyAspLysThrLysCysPhe 220
DB      806 GAGGAACGTGGCAGAGCCGGAATTCCTTAACAAGCCAAAGTGACGTTCCGTGGAAACAGCAGCC 865
QY      221 TyrCysAspGlyGlyLeuLysAspTrpGluSerAspAspValProTrpGluGlnHisAla 240
DB      866 TATTGCGACGAGGGCTTAAAGATTGGGAAAGCGATGACGTTCCGTGGAAACAGCAGCC 925
QY      241 ArgTrpPheAspArgCysAlaTyrValGlnLeuValLysGlyArgAspTyrIleGlnLys 260
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QY      321 AlaLysCysAlaLeuSerThrAspLysCysProMetCysArgArgThrPheThrAsnAla 340
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RESULT 2

US-10-267-502-202
; Sequence 202, Application US/10267502
; Publication No. US20040071700A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jaeseob
; APPLICANT: Galant, Ron
; TITLE OF INVENTION: Obesity Linked Genes
; FILE REFERENCE: LSD-07416
; CURRENT APPLICATION NUMBER: US/10/267,502
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 202
; LENGTH: 1317
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-10-267-502-202

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US-10-041-859-2 (1-346) x US-10-267-502-202 (1-1317)

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	725.5	38.4	1317	US-09-586-305A-2	Sequence 2, Appli
4	723.5	38.3	1317	US-09-586-305A-1	Sequence 1, Appli
5	723.5	38.3	1317	US-09-586-305A-3	Sequence 3, Appli
6	717.5	38.0	1317	US-09-586-305A-4	Sequence 4, Appli
7	717.5	38.0	1317	US-09-586-305A-5	Sequence 5, Appli
8	715.5	37.9	1317	US-09-586-305A-9	Sequence 9, Appli
9	713.5	37.8	1317	US-09-586-305A-10	Sequence 10, Appli
10	712.5	37.8	1317	US-09-586-305A-6	Sequence 6, Appli
11	712.5	37.8	1317	US-09-586-305A-7	Sequence 7, Appli
12	704	37.3	1304	US-09-586-305A-8	Sequence 8, Appli

13	526.5	27.9	2563	4	US-09-016-434-1076	Sequence 1076, Ap
14	526.5	27.9	2563	4	US-09-023-655-894	Sequence 894, App
15	526.5	27.9	2601	3	US-08-569-749-3	Sequence 3, Appli
16	526.5	27.9	2601	5	PCT-US96-12860-3	Sequence 3, Appli
17	526.5	27.9	3076	2	US-09-205-144-1	Sequence 1, Appli
18	526.5	27.9	3076	4	US-09-814-915A-11	Sequence 11, Appli
19	525.5	27.8	2676	3	US-09-212-971-11	Sequence 11, Appli
20	525.5	27.8	2676	3	US-08-800-929A-11	Sequence 11, Appli
21	525.5	27.8	2676	3	US-09-617-053A-11	Sequence 11, Appli
22	525.5	27.8	6669	3	US-09-212-971-5	Sequence 5, Appli
23	525.5	27.8	6669	3	US-08-800-929A-5	Sequence 5, Appli
24	525.5	27.8	6669	3	US-09-617-053A-5	Sequence 5, Appli
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26	524.5	27.8	2676	2	US-08-511-485-5	Sequence 5, Appli
27	524.5	27.8	2676	4	US-09-201-936-5	Sequence 5, Appli
28	524.5	27.8	2676	4	US-09-011-356-5	Sequence 5, Appli
29	524.5	27.8	2676	4	US-09-672-717-220	Sequence 220, App
30	524.5	27.8	2676	4	US-09-201-932-5	Sequence 5, Appli
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32	517.5	27.4	2450	4	US-09-201-936-39	Sequence 39, Appli
33	517.5	27.4	2450	4	US-09-201-932-39	Sequence 39, Appli
34	517.5	27.4	2474	4	US-09-011-356-39	Sequence 39, Appli
35	517.5	27.4	2474	4	US-09-672-717-226	Sequence 226, App
36	507.5	26.9	2580	2	US-08-511-485-7	Sequence 7, Appli
37	507.5	26.9	2580	4	US-09-201-936-7	Sequence 7, Appli
38	507.5	26.9	2580	4	US-09-011-356-7	Sequence 7, Appli
39	507.5	26.9	2580	4	US-09-672-717-222	Sequence 222, App
40	507.5	26.9	2580	4	US-09-201-932-7	Sequence 7, Appli
41	500.5	26.5	2589	3	US-08-569-749-1	Sequence 1, Appli
42	500.5	26.5	2589	5	PCT-US96-12860-1	Sequence 1, Appli
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44	500.5	26.5	3732	3	US-09-212-971-7	Sequence 7, Appli
45	500.5	26.5	3732	3	US-08-800-929A-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-502-528-2
; Sequence 2, Application US/09502528
; Patent No. 6570069
; GENERAL INFORMATION:
; APPLICANT: Hammock, Bruce D.
; APPLICANT: Huang, Qihong
; APPLICANT: Maeda, Susumu
; TITLE OF INVENTION: The Regents of the University of California
; FILE REFERENCE: 023070-112000US
; CURRENT APPLICATION NUMBER: US/09/502,528
; CURRENT FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1134
; TYPE: DNA
; ORGANISM: Spodoptera frugiperda
; FEATURE:
; OTHER INFORMATION: SFIAP nucleotide sequence, open reading frame
; NAME/KEY: CDS
; LOCATION: (1)..(1134)
; OTHER INFORMATION: fail armyworm inhibitor of apoptosis protein
; OTHER INFORMATION: (SFIAP)
US-09-502-528-2

Alignment Scores:
Pred. No.: 2.38e-132
Score: 1311.00
Percent Similarity: 79.28%
Best Local Similarity: 68.51%
Query Match: 69.48%
DB: 4
Length: 1134
Matches: 248
Conservative: 39
Mismatch: 57
Indels: 18
Gaps: 7

US-10-041-859-2 (1-346) x US-09-502-528-2 (1-1134)

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QY      1 MetGluLeuThrIysValAlaIlyAsnGlyAlaAlaIaThrLeuValMetLeuIysAsn 20
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QY      21 ---AlaArgAspAlaIlyMetArgProPheIleGlyProLeuMetLeu-----SerSer 37
DB      112 GGATCGCTTGAGGCTAAATTCGACCT---CTCGCGCCACTAATGCTGCGCAGCCCAAGT 168
QY      38 CysGluSerSerThrThrSerThrLeuProSerProSerSer----- 51
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QY      71 MetArgArgGluGluGluArgLeuIysThrPheAspGlnTrpProValThrPheLeuThr 90
DB      289 ATGAGAAAAGAGGATGACGATGAAAAACATTTGAAAAATGCCCGTAAGTTTCTATCC 348
QY      91 ProGluGlnLeuAlaArgAsnGlyPheTyrTyrLeuGlyArgGlyAspGluValCysCys 110
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QY      111 AlaPheCysLysValGluIleMetArgTrpValGluGlyAspAspProAlaAlaAspHis 130
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QY      131 ArgArgTrpAlaProGlnCysProPheValArgLysGlnMetTyrAlaAsnAlaGlyGly 150
DB      469 CAGCGTTGGGCGCCACAGTGCCTATTGTGCGCAAA---TTGAACGGTACTGCAGCAGCA 525
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QY      188 ThrPheLysAspTrpProArgArgMetArgGlnLysProGluGlnLeuAlaGluAlaGly 207
DB      646 AGTTTAAAGACTGGCCACGATGCATGCAACAAAACCTGAAGACTCGCCGAGGCTGCG 705
QY      208 PhePheTyrThrGlyGlnGlyAspLysThrLysCysPheTyrCysAspGlyGlyLeuLys 227
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QY      228 AspTrpGluSerAspAspValProTrpGluGlnHisAlaArgTrpPheAspArgCysAla 247
DB      766 GATTGGAGAAACCATGACGTACCTTGGGAACAACACGCAAGGTGTTGACCGTTGCGCC 825
QY      248 TyrValGlnLeuValLysGlyArgAspTyrIleGlnLysValLysSerGluAlaThrAla 267
DB      826 TACGTGCAATTGGTGAAGGTCGAAATACGTTCAAAAGGTGATTTCTGAAGCTTGAG 885
QY      268 IleSerAlaSerGluGluGln-----AlaAlaThrAsnAspSerThrLysAsn 284
DB      886 GTATCCGCGTCAGAAAGCGGAACGTGATAGCAACCCGCAAGGACTCGCCGAGCCCAAGCCG 945
QY      285 ValAlaGlnGluGlyLysLysLeuAspAspSerLysIleCysLysIleCysTyrSer 304
DB      946 CCAAGCAGAGCGCCGCAAGAAACCTCACTGATCAAAAGTTGTAAAAATCTGTTATGCT 1005
QY      305 GluGluArgAsnValCysPheValProCysGlyHisValAlaAlaCysAlaLysCysAla 324
DB      1006 GAAGAGCGTAACTGTGCTTGTGCTGCGCGCCGACGTTGCTGCGCCCAAGTGGCG 1065
QY      325 LeuSerThrAspLysCysProMetCysArgArgThrPheThrAsnAlaValArgLeuTyr 344
DB      1066 CTGCGCGCGCCGACAAAGTGCCTCATGTGCGCAGAGACGTTTCAAAATGACAGTGCCTTATAT 1125

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QY      345 PheSer 346
DB      1126 TTCTCG 1131

RESULT 2
US-09-502-528-1
; Sequence 1, Application US/09502528
; Patent No. 6570069
; GENERAL INFORMATION:
; APPLICANT: Hammock, Bruce D.
; APPLICANT: Huang, Qihong
; APPLICANT: Maeda, Susumu
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Inhibitors of Apoptosis
; FILE REFERENCE: 023070-112000US
; CURRENT APPLICATION NUMBER: US/09/502,528
; CURRENT FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1739
; TYPE: DNA
; ORGANISM: Spodoptera frugiperda
; FEATURE:
; OTHER INFORMATION: fall armyworm inhibitor of apoptosis protein
; OTHER INFORMATION: (SfiAP) nucleotide sequence including 5' and 3'
; NAME/KEY: CDS
; LOCATION: (229)..(1362)
; OTHER INFORMATION: fall armyworm inhibitor of apoptosis protein
; OTHER INFORMATION: (SfiAP)
US-09-502-528-1

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Alignment Scores:

	Pred. No.:	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
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US-10-041-859-2 (1-346) x US-09-502-528-1 (1-1739)
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DB      340 GGATCGCTTGAGGCTTAAATTCGACCT---CTCGCGCCACTAATGCTGCCGACGCCAAGT 396
QY      38 CysGluSerSerThrThrSerThrLeuProSerProSerSer----- 51
DB      397 TACGACTCCAACGCCGCTCTCCATCTTGTCTCCATCCACGCTTGCTCTTCACTTCT 456
QY      52 ---SerAlaAspLysThrAspAsnHisAspThrPheAsnPhelLeuProAspMetProAsp 70
DB      457 TTCTCCATTGATAAAAACGACAACCAACGACACCTTCGCGCTTCAGTGCAGACAGATTGAT 516
QY      71 MetArgArgGluGluGluArgLeuIysThrPheAspGlnTrpProValThrPheLeuThr 90
DB      517 ATGAGAAAAGAGGATGAACGTATGAAAAACATTTGAAAAATGGCCCGTAAGTTTCTATCC 576
QY      91 ProGluGlnLeuAlaArgAsnGlyPheTyrTyrLeuGlyArgGlyAspGluValCysCys 110
DB      577 GGAGAGCAACTTGCTCGAATGATTTACTTACCTCGCGCGTAGAGATGAAGCCCGTTGC 636
QY      111 AlaPheCysLysValGluIleMetArgTrpValGluGlyAspAspProAlaAlaAspHis 130
DB      637 GCTTCTGTTAAAGTGAGATTATGAGTGGGTGGAAGGCGCATGACCCCTGCAAGACCAT 696
QY      131 ArgArgTrpAlaProGlnCysProPheValArgLysGlnMetTyrAlaAsnAlaGlyGly 150

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 13, 2005, 13:35:09 ; Search time 569 Seconds
(without alignments)
3192.091 Million cell updates/sec

Title: US-10-041-859-2
Perfect score: 1887
Sequence: 1 MELTKVAKNGAATLVMLKN.....TDKCPMCRRTFTNAVRLYFS 346

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
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Searched: 413486 seqs, 2624710521 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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Database : N_Geneseq_23Sep04:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1887	100.0	3773	6	ABQ78228
2	1311	69.5	1739	5	AAD14419
3	787	41.7	5000	6	ABL55643
4	748	39.6	794	6	ABL55635
5	721.5	38.2	1317	5	AAC84521
6	719.5	38.1	1317	5	AAC84520

7	719.5	38.1	1317	5	AAC84522	Aac84522 Drosophil
8	719.5	38.1	1317	12	ADO07876	Ado07876 Fly polyn
9	719.5	38.1	1858	4	ABL21061	Ab121061 Drosophil
10	719.5	38.1	2013	4	ABL10083	Ab110083 Drosophil
11	719.5	38.1	10432	4	ABL10082	Ab110082 Drosophil
12	719.5	38.1	14250	4	ABL21060	Ab121060 Drosophil
13	713.5	37.8	1317	5	AAC84523	Aac84523 Drosophil
14	713.5	37.8	1317	5	AAC84524	Aac84524 Drosophil
15	711.5	37.7	1317	5	AAC84528	Aac84528 Drosophil
16	709.5	37.6	1317	5	AAC84529	Aac84529 Drosophil
17	708.5	37.5	1317	5	AAC84525	Aac84525 Drosophil
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19	700	37.1	1304	5	AAC84527	Aac84527 Drosophil
20	546.5	29.0	131680	10	ADF29092	Adf29092 Agrotis s
21	526.5	27.9	2563	9	ADB80989	Adb80989 RING-SH c
22	526.5	27.9	2563	10	ACA56478	Aca56478 Human sig
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30	526.5	27.9	3076	6	ABL66325	Ab166325 Lung canc
31	526.5	27.9	3076	8	ABX10968	Abx10968 CDNA enco
32	526.5	27.9	3076	10	AAD60472	Aad60472 Human cel
33	526.5	27.9	3164	8	ABV75363	Abv75363 Human CIA
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35	526.5	27.9	3165	12	ADH74642	Adh74642 CDNA enco
36	526.5	27.9	5212	8	ABX10333	Abx10333 DNA enco
37	526.5	27.9	5844	10	ADB47553	Adb47553 Human cdn
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ALIGNMENTS

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ID	ABQ78228 standard; CDNA; 3773 BP.
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AC	ABQ78228;
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DT	22-OCT-2002 (first entry)
XX	
DE	Nucleotide sequence of inhibitor of apoptosis protein BmiAP.
XX	
KW	Inhibitor of apoptosis protein; IAP; BmiAP; silkworm; apoptosis; insect;
XX	
KW	Spodoptera frugiperda; insult-resistant plant; caspase; gene; ss.
XX	
OS	Bombyx mori.
XX	
FH	Key
FT	CDs
FT	2733 . 3773
FT	Location/Qualifiers
FT	/*tag= a
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XX	
PN	WO200253586-A2.
XX	
PD	11-JUL-2002.
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PF	07-JAN-2002; 2002WO-US000314.
XX	
PR	08-JAN-2001; 2001US-0260478P.
XX	
PA	(BURN-) BURNHAM INST.
XX	

PI Maeda S, Huang Q, Reed JC, Deveraux QL;
XX WPI; 2002-590628/63.
DR P-PSDB; ABB78046.
XX
PT Novel recombinant polypeptide, inhibitor of apoptosis protein family
PT member BmiAP from silkworm Bombyx mori BmN cells, useful for inhibiting
PT apoptosis and identifying an agent that modulates activity of
PT polypeptide.
XX
PS Claim 8; Page 29-30; 62pp; English.
XX
CC The present scone encodes a polypeptide which is an inhibitor of
CC apoptosis protein (IAP) family member, and designated BmiAP. BmiAP is
CC derived from silkworm Bombyx mori BmN cells. The BmiAP polypeptide
CC contains two baculoviral IAP repeat (BIR) domains, followed by a RING
CC domain. BmiAP polypeptides and polynucleotides are useful for inhibiting
CC apoptosis in insect cells, especially Spodoptera frugiperda or Bombyx
CC mori cells, and mammalian cells, and plant cells. They are also useful
CC for generating a biotic or abiotic insult-resistant plant. BmiAP is also
CC useful for inhibiting caspases
XX

SQ Sequence 3773 BP; 1108 A; 785 C; 866 G; 1014 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.27e-168	Length:	3773
Score:	1887.00	Matches:	346
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
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US-10-041-859-2 (1-346) x ABQ78228 (1-3773)

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DB 326 TCAACGACATCCACACTCCCGTCACCTTCGTCTGCTGAGCTGATTAACGATATACGAC 385
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DB 446 TTTGATCATGTGCCCGTTACGTTTGTGACGCCGGAACAATTGGCCCGCAACGATTCTAC 505
QY 101 TyrLeuGlyArgGlyAspGluValCysCysAlaPheCysLysValGluIleMetArgTrp 120
DB 506 TACCTCGGTGCGCGGACGAAAGTGTGCTTTCTGTAAAGTAGAAATTATGAGGTGG 565
QY 121 ValGluGlyAspAspProAlaAlaAspHisArgArgTrpAlaProGlnCysProPheVal 140
DB 566 GTCGAAGCGACGATCTCTGCCCGCATCATCGAGATGGCGCCCAAGTGTCCCTTTGTA 625
QY 141 ArgLysGlnMetTyrAlaAsnAlaGlyGlyAlaThrAlaValGlyArgAspGluCys 160
DB 626 CGAAAACAAATGTATGCCAACGCTGGGGGAGAGGCGAACCGCTGTGCTAGAGACGAATGT 685
QY 161 GlyAlaSerAlaAlaThrGlnProProArgMetProGlyProValHisAlaArgTyrSer 180
DB 686 GGGGCCAGTGGCCACGACGAGCTTCCCGCATGCCCCGGCGCCGCGGTACTCC 745
QY 181 ThrGluAlaAlaArgLeuAlaThrPheLysAspTrpProArgArgMetArgGlnLysPro 200
DB 746 ACCGAGCGCGCGGCTCGCACCTTCAAGACTGCGCGAGACGTATGCGCCAAAAAACC 805

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QY 221 TyrCysAspGlyGlyLeuLysAspTrpGluSerAspAspValProTrpGluGlnHisAla 240
DB 866 TATTGCGACGAGGCGCTAAAGATTGGGAAAGCGATGACGTCCGTGGGACACGACGCC 925
QY 241 ArgTrpPheAspArgCysAlaTyrValGlnLeuValLysGlyArgAspTyrIleGlnLys 260
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QY 261 ValLysSerGluAlaThrAlaIleSerAlaSerGluGluGlnAlaAlaThrAsnAsp 280
DB 986 GTGAAGTCGAGGCCACTGCGATATCTGCTAGCGAAGAACAGGCCGCCACCAATGAT 1045
QY 281 SerThrLysAsnValAlaGlnGluGlyGluLysHisLeuAspAspSerLysIleCysLys 300
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DB 1226 GTGCGGCTTACTTCTCG 1243

RESULT 2

AAD14419

ID AAD14419 standard; cDNA; 1739 BP.

XX AAD14419;

DT 01-NOV-2001 (first entry)

DE Fall armyworm inhibitor of apoptosis (IAP) cDNA.

XX Fall armyworm; inhibitor of apoptosis; IAP; transgenic plant;
KW apoptosis inhibitor; therapy; acquired immune deficiency syndrome; AIDS;
KW neurodegenerative disease; Alzheimer's disease; aplastic anaemia;
KW Parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa;
KW myelodysplastic syndrome; toxin-induced liver disease; ischaemic injury;
KW myocardial infarction; stroke; reperfusion injury; cancer; neotropic;
KW autoimmune disorder; lupus erythematosus; multiple sclerosis; vasotropic;
KW insecticide; viral infection; anti-HIV; human immunodeficiency virus;
KW neuroprotective; antianaemic; cardiant; cerebroprotective; vulnerary;
KW cyostatic; immunosuppressive; virucide; antialcoholic; BS.

OS Spodoptera frugiperda.

FH Key Location/Qualifiers

FT CDS 229..1362

FT /tag= a
FT /product= "inhibitor of apoptosis protein"
FT /note= "CDS is referred as SEQ ID NO 2 in the
FT specification"

XX WO200159108-A2.

PD 16-AUG-2001.

PF 07-FEB-2001; 2001WO-US004071.

PR 10-FEB-2000; 2000US-00502528.

XX (REGC) UNIV CALIFORNIA.

PA (MAED/) MAEDA H.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 6, 2005, 19:29:14 ; Search time 148 Seconds
(without alignments)
842.957 Million cell updates/sec

Title: US-10-041-859-2

Perfect score: 1887

Sequence: 1 MELTKVAKNGAATLVMLKN.....TDKCPMCRFTFTNAVRLYFS 346

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1603904 seqs, 360571292 residues

Total number of hits satisfying chosen parameters: 1603904

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1887	100.0	346	14	US-10-041-859-2 Sequence 2, Appli
2	966	51.2	275	9	US-09-201-936-12 Sequence 12, Appl
3	966	51.2	275	14	US-10-323-643-9 Sequence 9, Appli
4	966	51.2	275	16	US-10-600-272-12 Sequence 12, Appl
5	932.5	49.4	172	14	US-10-041-859-8 Sequence 8, Appli
6	862	45.7	268	14	US-10-323-643-10 Sequence 10, Appl
7	846.5	44.9	172	14	US-10-041-859-10 Sequence 10, Appl
8	831.5	44.1	172	14	US-10-041-859-9 Sequence 9, Appli
9	759.5	40.2	172	14	US-10-041-859-11 Sequence 11, Appl
10	719.5	38.1	438	15	US-10-267-502-419 Sequence 419, App
11	696.5	36.9	172	14	US-10-041-859-12 Sequence 12, Appl
12	554.5	29.4	172	14	US-10-041-859-13 Sequence 13, Appl
13	526.5	27.9	604	14	US-10-232-286-4 Sequence 4, Appli

14	526.5	27.9	604	14	US-10-141-618-6	Sequence 6, Appli
15	526.5	27.9	604	14	US-10-366-307-6	Sequence 6, Appli
16	526.5	27.9	604	16	US-10-730-476A-79	Sequence 79, Appl
17	526.5	27.9	604	17	US-10-825-282-40	Sequence 40, Appl
18	525.5	27.8	600	9	US-09-974-592-12	Sequence 12, Appl
19	525.5	27.8	600	17	US-10-482-952-1	Sequence 1, Appli
20	524.5	27.8	604	9	US-09-974-592-6	Sequence 6, Appli
21	524.5	27.8	604	9	US-09-201-936-6	Sequence 6, Appli
22	524.5	27.8	604	16	US-10-636-065-221	Sequence 221, App
23	524.5	27.8	604	16	US-10-600-272-6	Sequence 6, Appli
24	517.5	27.4	602	9	US-09-201-936-40	Sequence 40, Appl
25	517.5	27.4	602	16	US-10-636-065-227	Sequence 227, App
26	517.5	27.4	602	16	US-10-600-272-40	Sequence 40, Appl
27	507.5	26.9	618	9	US-09-974-592-8	Sequence 8, Appli
28	507.5	26.9	618	9	US-09-201-936-8	Sequence 8, Appli
29	507.5	26.9	618	16	US-10-636-065-223	Sequence 223, App
30	507.5	26.9	618	16	US-10-600-272-8	Sequence 8, Appli
31	500.5	26.5	498	9	US-09-201-936-13	Sequence 13, Appl
32	500.5	26.5	498	16	US-10-600-272-13	Sequence 13, Appl
33	500.5	26.5	618	14	US-10-153-668-338	Sequence 338, App
34	500.5	26.5	618	14	US-10-207-655-200	Sequence 200, App
35	500.5	26.5	618	14	US-10-232-286-2	Sequence 2, Appli
36	500.5	26.5	618	14	US-10-366-307-4	Sequence 4, Appli
37	500.5	26.5	618	15	US-10-361-270-3	Sequence 3, Appli
38	500.5	26.5	618	15	US-10-260-708-63	Sequence 63, Appl
39	500.5	26.5	618	16	US-10-730-476A-78	Sequence 78, Appl
40	500.5	26.5	618	17	US-10-482-952-11	Sequence 11, Appl
41	499.5	26.5	497	14	US-10-366-307-2	Sequence 2, Appli
42	497.5	26.4	497	9	US-09-974-592-4	Sequence 4, Appli
43	497.5	26.4	497	9	US-09-201-936-4	Sequence 4, Appli
44	497.5	26.4	497	16	US-10-636-065-219	Sequence 219, App
45	497.5	26.4	497	16	US-10-600-272-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-10-041-859-2
; Sequence 2, Application US/10041859
; Publication No. US20030049796A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, QIHONG
; APPLICANT: REED, JOHN C.
; APPLICANT: DEVERAUX, QUINN L.
; APPLICANT: MAEDA, SUSUMU
; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND
; FILE REFERENCE: 087102/027 2537
; CURRENT APPLICATION NUMBER: US/10/041, 859
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260, 478
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Bombyx mori
US-10-041-859-2

Query Match 100.0%; Score 1887; DB 14; Length 346;
Best Local Similarity 100.0%; Pred. No. 1.7e-169;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MELTKVAKNGAATLVMLKNARDAKMRPFIGPLMLSSCESTSTLPSPSSADXTDND 60
Db 1 MELTKVAKNGAATLVMLKNARDAKMRPFIGPLMLSSCESTSTLPSPSSADXTDND 60
QY 61 TFNFLPDMRREERLKTFTDQWPVFTLTPEQLARNGFYLLGRGDEVCCARCKVEIMRW 120
Db 61 TFNFLPDMRREERLKTFTDQWPVFTLTPEQLARNGFYLLGRGDEVCCARCKVEIMRW 120

QY	121	VEGDDPADHRRWAPQCPFVVRKQMYANAGSEATAVGRDECGASATQPPRMGPVHARYS	180
Db	121	VEGDDPADHRRWAPQCPFVRKQMYANAGSEATAVGRDECGASATQPPRMGPVHARYS	180
QY	181	TEARLATFKDWPRRMRQKPEELAEAGFYTGQDGTKCFYCDGGLKDWESDVPWEQHA	240
Db	181	TEARLATFKDWPRRMRQKPEELAEAGFYTGQDGTKCFYCDGGLKDWESDVPWEQHA	240
QY	241	RMFDRCAVYQLVKGRDYIQVKSEATAISASEEQATNDSTKNVAQEGEKHLDSKIC	300
Db	241	RMFDRCAVYQLVKGRDYIQVKSEATAISASEEQATNDSTKNVAQEGEKHLDSKIC	300
QY	301	ICYSEERNVCFVPCGHVAVACAKALSTDKCPMCRRTFTNAVRLYFS	346
Db	301	ICYSEERNVCFVPCGHVAVACAKALSTDKCPMCRRTFTNAVRLYFS	346

RESULT 2

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US-09-201-936-12
; Sequence 12, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201, 936
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011, 356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576, 956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511, 485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Cydia pomonella
US-09-201-936-12

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Query Match 51.2%; Score 966; DB 9; Length 275;

Best Local Similarity 59.2%; Pred. No. 1.3e-82;
Matches 171; Conservative 39; Mismatches 55; Indels 24; Gaps 3;

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QY	128	ADHRRWAPQCPFVRKQMYANAGGEATAVGRDECGASAATQ-----PRMPGPVHARYS	180
Db	61	ADHKKWAPQCPFEVK-----GIDVCGSIVTTNNIQTTHDTIIGRAHPKXA	106
QY	181	TEAARLATEFKDMPRRMRQKPEBLAEAGFFYTGGDKTCFYCDGGLKDWESDVPMEQHA	240
Db	107	HEAARVKSFNHWPBRCMKQRPQOMADAGFFYTGYGNTKCFYCDGGLKDWEPEDVPMEGHV	166
QY	241	RMFDRCAYVQLVKGRDYIQVKSEATAI---SASEEQAAITNDSTKNVAQEGEKHLDDSK	297
Db	167	RMFDRCAYVQLVKGRDYQKVITTEACVLPGENTIVSTAAPVSEPIPETKIEKEPQVEDSK	226
QY	298	ICKICYSEERNVCFVPCGHVAVACAKCALSTDKCPMCRRTFTNAVRLYFS	346
Db	227	LCKICYBECIVCFVPCGHVAVACAKCALSVDKCPMCRKIVTSVLKVYFS	275

RESULT 3

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US-10-323-643-9
; Sequence 9, Application US/10323643
; Publication No. US20030108552A1
; GENERAL INFORMATION:
; APPLICANT: He, et al.
; TITLE OF INVENTION: Human Inhibitor of Apoptosis Gene 1
; FILE REFERENCE: PF165P1D1
; CURRENT APPLICATION NUMBER: US/10/323,643
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 08/464,588
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US95/05922
; PRIOR FILING DATE: 1995-05-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Cydia pomonella granulovirus
US-10-323-643-9

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Query Match 51.2%; Score 966; DB 14; Length 275;

Best Local Similarity 59.2%; Pred. No. 1.3e-82;
Matches 171; Conservative 39; Mismatches 55; Indels 24; Gaps 3;

QY	68	MDMRREERLKTFDQMPVTELTPEQLARNGFYLLGRGDEVCCAFCKVEIMRWEGDDPA	127
Db	1	MSDLRLIEVRLNTFEKWPVPSFLSPETMAKNGFYLLGRSDEVRCACFKVEIMRWEGEDPA	60
QY	128	ADHRWAPOCFVRKQMYANAGGEATAVGRDECGASAATQ-----PPRMGPVHARYS	180
Db	61	ADHKWAPQCPFVK-----GIDVCGSIVTTNNIQTTHDTTIGBAHPKYA	106
QY	181	TEARLATFKDMPRRMQPEELAEAGFFYTGQDKTKCFYCDGGLKDWESDDVPWEQHA	240
Db	107	HEARVKSFPNNPRCMKQRPQOMADAGFFYTGXDNTKCFYCDGGLKDWEPEDVPWEQHV	166
QY	241	RMPDRCAIVQLVKGRDYIQVKSEATAI---SASEEQATNDSTKNVAQEGEKHLDDSK	297
Db	167	RMFDRCAIVQLVKGRDYQKVITAEACVLPGENTTVSTAAPVSEPIPETKIEKEPQVEDSK	226
QY	298	ICKICYSEERNVCFVPCGHVAVACAKCALSTDKCPMCRRTFTNAVRLYES	346
Db	227	LCKICYVEECIVCFVPCGHVAVACAKCALSDVKCPMCRKIIVTSVLKVYES	275

RESULT 4

US-10-600-272-12
; Sequence 12, Application US/10600272

Publication No. US20040157232A1
; GENERAL INFORMATION:

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1  APPLICANT: Korneluk, Robert G.
2  APPLICANT: Mackenzie, Alexander E.
3  APPLICANT: Baird, Stephen
4  APPLICANT: Liston, Peter
5  TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS
6  TITLE OF INVENTION: PROBES, AND DETECTION METHODS
7  FILE REFERENCE: 07891/003006
8  CURRENT APPLICATION NUMBER: US/10/600,272
9  CURRENT FILING DATE: 2003-06-20
10 PRIOR APPLICATION NUMBER: US 09/011,356
11 PRIOR FILING DATE: 1998-02-04
12 PRIOR APPLICATION NUMBER: PCT/IB96/01022
13 PRIOR FILING DATE: 1996-08-05
14 PRIOR APPLICATION NUMBER: US 08/576,956
15 PRIOR FILING DATE: 1995-12-22
16 PRIOR APPLICATION NUMBER: US 08/511,485
17 PRIOR FILING DATE: 1995-08-04
18 NUMBER OF SEQ ID NOS: 45
19 SOFTWARE: FastSeq for Windows Version 4.0
20 SEQ ID NO 12
21 LENGTH: 275
22 TYPE: PRT

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2005, 18:43:17 ; Search time 30 Seconds
(without alignments)
764.868 Million cell updates/sec

Title: US-10-041-859-2

Perfect score: 1887

Sequence: 1 MELTKVAKNGAATLVMLKN.....TDKCPMCRRFTTNAVRLYFS 346

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	966	51.2	275	3	US-08-836-134-21
4	966	51.2	275	4	US-09-493-784-21
5	966	51.2	275	4	US-09-201-936-12
6	966	51.2	275	4	US-09-011-356-12
7	966	51.2	275	4	US-09-201-932-12
8	862	45.7	268	3	US-08-836-134-22
9	862	45.7	268	4	US-09-493-784-22
10	725.5	38.4	438	4	US-09-586-305A-12
11	723.5	38.3	438	4	US-09-586-305A-11
12	723.5	38.3	438	4	US-09-586-305A-13
13	717.5	38.0	438	4	US-09-586-305A-14
14	717.5	38.0	438	4	US-09-586-305A-15
15	715.5	37.9	438	4	US-09-586-305A-19
16	713.5	37.8	438	4	US-09-586-305A-20
17	712.5	37.8	438	4	US-09-586-305A-16
18	712.5	37.8	438	4	US-09-586-305A-17
19	531.5	28.2	431	4	US-09-586-305A-18
20	526.5	27.9	604	3	US-08-569-749-4
21	526.5	27.9	604	5	PCT-US96-12860-4
22	525.5	27.8	600	3	US-09-212-971-12
23	525.5	27.8	600	3	US-08-800-929A-12
24	525.5	27.8	600	3	US-09-617-053A-12
25	524.5	27.8	604	2	US-08-511-485-6
26	524.5	27.8	604	3	US-09-212-971-6
27	524.5	27.8	604	3	US-08-800-929A-6

28	524.5	27.8	604	3	US-09-617-053A-6	Sequence 6, Appli
29	524.5	27.8	604	4	US-09-201-936-6	Sequence 6, Appli
30	524.5	27.8	604	4	US-09-011-356-6	Sequence 6, Appli
31	524.5	27.8	604	4	US-09-672-717-221	Sequence 221, App
32	524.5	27.8	604	4	US-09-201-932-6	Sequence 40, Appl
33	517.5	27.4	602	4	US-09-011-356-40	Sequence 40, Appl
34	517.5	27.4	602	4	US-09-672-717-227	Sequence 40, Appl
35	517.5	27.4	602	4	US-09-201-932-40	Sequence 227, App
36	517.5	26.9	618	2	US-08-511-485-8	Sequence 8, Appli
37	507.5	26.9	618	3	US-09-212-971-8	Sequence 8, Appli
38	507.5	26.9	618	3	US-08-800-929A-8	Sequence 8, Appli
39	507.5	26.9	618	3	US-09-617-053A-8	Sequence 8, Appli
40	507.5	26.9	618	4	US-09-201-936-8	Sequence 8, Appli
41	507.5	26.9	618	4	US-09-011-356-8	Sequence 8, Appli
42	507.5	26.9	618	4	US-09-672-717-223	Sequence 223, App
43	507.5	26.9	618	4	US-09-201-932-8	Sequence 8, Appli
44	507.5	26.9	618	4	US-08-657-759-1	Sequence 1, Appli
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ALIGNMENTS

RESULT 1
US-09-502-528-3
; Sequence 3, Application US/09502528
; Patent No. 6570069
; GENERAL INFORMATION:
; APPLICANT: Hammock, Bruce D.
; APPLICANT: Huang, Qihong
; APPLICANT: Maeda, Susumu
; TITLE OF INVENTION: The Regents of the University of California
; FILE REFERENCE: 023070-112000US
; CURRENT APPLICATION NUMBER: US/09/502, 528
; CURRENT FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Spodoptera frugiperda
; FEATURE:
; OTHER INFORMATION: fall armyworm inhibitor of apoptosis protein
; US-09-502-528-3

QY	1	MELTKVAKNGAATLVMLKN-ARDAKMRPFIGPLML--SSCESSTSTLPSPSS-----	51
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QY	52	-SADKTDNHDTFNPLPDMRREERLKTFDQWPVTLTPEQLARNGFYILGRDEVCC	110
Db	77	FSIDKTDNHDTFGFSADTVDMRKEDERMKTFEKWPVSFLSGEQLARNGFYILGRDEARC	136
QY	111	AFCKVEIMRWVEGDDPAADHRRWAPQCFVVRKQMYANAGGEATAVGRDECGASAA---TQ	167
Db	137	AFCKVEIMRWVEGDDPAADHRRWAPQCFVVRK-LNGTAADTSSGQDECGARAAPSCTS	195
QY	168	PPRMGPVHARYSTEARLATFEKDWPRMRQKPEBELAEAGFFYTGQDKTKCFYCDGGLK	227
Db	196	PPRMAGPVHPRYASAEARLRSFKDWPRCMRQKPEBELAEAGFFYTGQDKTKCFYCDGGLK	255
QY	228	DWESDDVPWEQHARWFDRCAYVOLVKGRDYLQVKSEATAISASEEQ---AATNDSTKN	284
Db	256	DWENHDVPWEQHARWFDRCAYVOLVKGREYQKVISAECEVSASEAERDVAPARTAPESP	315
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Db	316	PAEAPENSVD	DKLCKICYAEERNVC	FVPCGHVACAKCALADKCPMCRRTFQNAVRLY	375
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RESULT 2

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US-08-511-485-12
; Sequence 12, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, F
; TITLE OF INVENTION: PROBES, AND DETECTION METHOD
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 275 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: both
; MOLECULE TYPE: protein
US-08-511-485-12

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Query Match	51.2%;	Score 966;	DB 2;	Length 275;
Best Local Similarity	59.2%;	Pred. No. 1e-92;		
Matches 171; Conservative	39;	Mismatches 55;	Indels 24;	Gaps 3;

QY		68	MPDMRREERLKTDPDQWPVTLTPEQLARNGEYLLGRGDEVCAFCCKVEIMRWEGEDBA	127
Dd		1	MSDLRLBEVRINTFEKWPVSFLSPETMAKNGFYYLGRSDEVRCAFCKVEIMRWKEGEDBA	60
QY		128	ADHRNNAPOCCEPVRKQOMYANAGGEATAVGRDECASAAQT-----PRMGPVHARYS	180
Dd		61	ADHKKAAPQCCPFVK-----GIDVCGSIVTTNNIQNTTHTTIIGPAHBKYA	106
QY		181	TEAARLATFKDWPRRRMRQKPEELAEAGFFYTGOGDTKTCFYCDGLKDWESDVPWEQHA	240
Dd		107	HEAARVKSFHNMWPRCMKQRPEQMADAGFFYTGYGDN TKCFYCDGLKDWE PEDVPWECHV	166
QY		241	RWFDRCAVVQLVKG RDI IQKVSEATAI---SASEEEQAATNDSTKNVAOEGEKHLDDSK	297
Dd		167	RWFDRCAVVQLVKG RDI YQKVIT EACVLPGENTTVSTADPVSEPIPETKIEKEPEVEDSK	226
QY		298	ICKICYSEERNVCFVPCGHVAVACA KALSTDCKCPMCRRFTTNNAVRLYFS	346

Db 227 LCKICVVEECIVCFVPCGHVAVACAKCALSDVKCPMCRKI VTSVLKVFS 275

RESULT 3

```

: Sequence 21, Application US/08836134A
: Patent No. 6020127
: GENERAL INFORMATION:
: APPLICANT: Mackenzie, Alex E.
: APPLICANT: Korneluk, Robert G.
: APPLICANT: Mahadevan, Mani S.
: APPLICANT: Mclean, Michael
: APPLICANT: Roy, Natalie
: APPLICANT: Ikeda, Joh-e
: TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence and
: Patent No. 6020127
: TITLE OF INVENTION: Mutations Causative of Spinal Muscular Atrophy
: FILE REFERENCE: 3477-112, 033477/139914
: CURRENT APPLICATION NUMBER: US/08/836,134A
: CURRENT FILING DATE: 1997-06-20
: NUMBER OF SEQ ID NOS: 23
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 21
: LENGTH: 275
: TYPE: PRT
: ORGANISM: Cydia pomonella
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: PCR primer
US-08-836-134-21

```

Query Match	51.2%;	Score 966;	DB 3;	Length 275;
Best Local Similarity	59.2%;	Pred. No. 1e-92;		
Matches 171;	Conservative 39;	Mismatches 55;	Indels 24;	Gaps 3;

[illegible]

RESULT 4

US-09-493-784-21
; Sequence 21, Application US/09493784
; Patent No. 6429011
; GENERAL INFORMATION:
; APPLICANT: Mackenzie, Alex E.
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mahadevan, Mani S.
; APPLICANT: McLean, Michael
; APPLICANT: Roy, Natalie
; APPLICANT: Ikeda, Joh-e
; TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence and
; Patent No. 6429011
; TITLE OF INVENTION: Mutations Causative of Spinal Muscular Atrophy
; FILE REFERENCE: 3477-112, 033477/139914
; CURRENT APPLICATION NUMBER: US/09/493,784
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 08/836,134

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 6, 2005, 19:39:50 ; Search time 154 Seconds
(without alignments)
805.976 Million cell updates/sec

Title: US-10-041-859-2

Perfect score: 1887

Sequence: 1 MELTKVAKNGAATLVMLKN.....TDKCPMCRRFTNAVLYFS 346

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1887	100.0	346	5	ABB78046	Abb78046 Amino ac
2	1311	69.5	377	4	AAE07881	Aae07881 Fall army
3	767.5	40.7	263	5	ABB09488	Abb09488 AMEPV bac
4	721.5	38.2	438	4	AAAB48189	Aab48189 Drosophil
5	719.5	38.1	438	4	ABB61858	Abb61858 Drosophil
6	719.5	38.1	438	4	ABB67347	Abb67347 Drosophil
7	719.5	38.1	438	4	AAAB48188	Aab48188 Drosophil
8	719.5	38.1	438	4	AAAB48190	Aab48190 Drosophil
9	719.5	38.1	438	8	ADCO08093	Adco08093 Fly polyp
10	713.5	37.8	438	4	AAAB48192	Aab48192 Drosophil
11	713.5	37.8	438	4	AAAB48191	Aab48191 Drosophil
12	711.5	37.7	438	4	AAAB48196	Aab48196 Drosophil
13	709.5	37.6	438	4	AAAB48197	Aab48197 Drosophil
14	708.5	37.5	438	4	AAAB48193	Aab48193 Drosophil
15	708.5	37.5	438	4	AAAB48194	Aab48194 Drosophil
16	532.5	28.2	434	4	AAAB48195	Aab48195 Drosophil
17	526.5	27.9	604	2	AAW19747	Aaw19747 Human inh
18	526.5	27.9	604	2	AAW13546	Aaw13546 Human c-I
19	526.5	27.9	604	2	AAV52703	Aav52703 Human cel
20	526.5	27.9	604	2	AAV33997	Aay33997 Human cel
21	526.5	27.9	604	6	ABU07431	Abu07431 Protein d
22	526.5	27.9	604	6	ABB82739	Abb82739 Human CIA
23	526.5	27.9	604	7	ADB80948	Adb80948 RING-SH c
24	526.5	27.9	604	7	AAE39811	Aae39811 Human cel
25	526.5	27.9	604	8	ADG87135	Adg87135 Human CIA

26	526.5	27.9	604	8	ADH74643	Adh74643 Human CIA
27	525.5	27.8	600	2	AAW69298	Aaw69298 Murine HI
28	525.5	27.8	600	6	ABP72155	Abp72155 Mouse inh
29	524.5	27.8	604	2	AAW19582	Aaw19582 Human apo
30	524.5	27.8	604	2	AAW69295	Aaw69295 Human HIA
31	524.5	27.8	604	5	ABG65664	Abg65664 Human inh
32	517.5	27.4	602	5	ABG65667	Abg65667 Mouse inh
33	516.5	27.4	602	2	AAW19585	Aaw19585 Mouse apo
34	507.5	26.9	618	2	AAW19583	Aaw19583 Human apo
35	507.5	26.9	618	2	AAW69296	Aaw69296 Human HIA
36	507.5	26.9	618	5	ABG65665	Abg65665 Human inh
37	501	26.6	497	7	ADI39803	Adi39803 Drosophil
38	500.5	26.5	496	2	AAW19745	Aaw19745 Mouse inh
39	500.5	26.5	618	2	AAW19746	Aaw19746 Human inh
40	500.5	26.5	618	2	AAW13545	Aaw13545 Human c-I
41	500.5	26.5	618	2	AAV33998	Aay33998 Human cel
42	500.5	26.5	618	6	ABP72160	Abp72160 Human inh
43	500.5	26.5	618	7	ADB80949	Adb80949 RING-SH c
44	500.5	26.5	618	7	ABR84600	AbR84600 IAP1 prot
45	500.5	26.5	618	7	ADD25639	Add25639 Binding d

ALIGNMENTS

RESULT 1	
ABB78046	
ID	ABB78046 standard; protein; 346 AA.
XX	
AC	ABB78046;
XX	
DT	22-OCT-2002 (first entry)
XX	
DE	Amino acid sequence of inhibitor of apoptosis protein BmiAP.
XX	
KW	Inhibitor of apoptosis protein; IAP; BmiAP; silkworm; apoptosis; insect;
KM	Spodoptera frugiperda; insult-resistant plant; caspase.
XX	
OS	Bombyx mori.
XX	
FH	Key
FT	Domain
FT	Domain
FT	Domain
FT	Domain
FT	Domain
FT	Domain
XX	
PN	WO200253586-A2.
XX	
PD	11-JUL-2002.
XX	
PF	07-JAN-2002; 2002WO-US000314.
XX	
PR	08-JAN-2001; 2001US-0260478P.
XX	
PA	(BURN-) BURNHAM INST.
XX	
PI	Maeda S, Huang Q, Reed JC, Deveraux QL;
XX	
DR	WPI, 2002-590628/63.
DR	N-PSDB; ABQ78228.
XX	
PT	Novel recombinant polypeptide, inhibitor of apoptosis protein family
PT	member BmiAP from silkworm Bombyx mori BmN cells, useful for inhibiting
PT	apoptosis and identifying an agent that modulates activity of
PT	polypeptide.
XX	
PS	Claim 39; Page 31; 62pp; English.
XX	
CC	The present score represents a polypeptide which is an inhibitor of
CC	apoptosis protein (IAP) family member, and designated BmiAP. BmiAP is
CC	derived from silkworm Bombyx mori BmN cells. The BmiAP polypeptide

CC contains two baculoviral IAP repeat (BIR) domains, followed by a RING
CC domain. BmiAP polypeptides and polynucleotides are useful for inhibiting
CC apoptosis in insect cells, especially Spodoptera frugiperda or Bombyx
CC mori cells, and mammalian cells, and plant cells. They are also useful
CC for generating a biotic or abiotic insul-resistant plant. BmiAP is also
CC useful for inhibiting caspases
XX
SQ Sequence 346 AA;

Query Match 100.0%; Score 1887; DB 5; Length 346;
Best Local Similarity 100.0%; Pred. No. 5.7e-174;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELTKVAKNGAAATLVMLKNARDAKMRPFIGPLMLSSCESSTSTLPSPSSADKTDNHD 60
Db 1 MELTKVAKNGAAATLVMLKNARDAKMRPFIGPLMLSSCESSTSTLPSPSSADKTDNHD 60
QY 61 TENFLPDMRREERLKTFDQWPVTLTPBQLARNGFYLLGRGDEVCCAFCKVEIMRW 120
Db 61 TENFLPDMRREERLKTFDQWPVTLTPBQLARNGFYLLGRGDEVCCAFCKVEIMRW 120
QY 121 VEGDDPADHRWAPQCPFVRKQMYANAGGEATAVGRDECGASAAATQPPRMPGPVHARYS 180
Db 121 VEGDDPADHRWAPQCPFVRKQMYANAGGEATAVGRDECGASAAATQPPRMPGPVHARYS 180
QY 181 TEARLATFKDWRMRMRQKPEELAEAGFFYTGQGDKTCKFYCDGGLKDWESDDVPWEQHA 240
Db 181 TEARLATFKDWRMRMRQKPEELAEAGFFYTGQGDKTCKFYCDGGLKDWESDDVPWEQHA 240
QY 241 RWFDRCAVQLVGRDYIQVKSEATAISASEEQATNDSTKNVAQEGEKHLDDSKICK 300
Db 241 RWFDRCAVQLVGRDYIQVKSEATAISASEEQATNDSTKNVAQEGEKHLDDSKICK 300
QY 301 ICYSEERNVCFVPGHVAVACAKALSTDKCPMCRRTFTNAVRLYFS 346
Db 301 ICYSEERNVCFVPGHVAVACAKALSTDKCPMCRRTFTNAVRLYFS 346

RESULT 2
AAE07881
ID AAE07881 standard; protein; 377 AA.
XX

AC AAE07881;
XX
DT 01-NOV-2001 (first entry)
XX

DE Fall armyworm inhibitor of apoptosis (IAP) protein.

KW Fall armyworm; inhibitor of apoptosis; IAP; transgenic plant;
KW apoptosis inhibitor; therapy; acquired immune deficiency syndrome; AIDS;
KW neurodegenerative disease; Alzheimer's disease; aplastic anaemia;
KW Parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa;
KW myelodysplastic syndrome; toxin-induced liver disease; ischaemic injury;
KW myocardial infarction; stroke; reperfusion injury; cancer; neotropic;
KW autoimmune disorder; lupus erythematosus; multiple sclerosis; vasculitic;
KW insecticide; viral infection; anti-HIV; human immunodeficiency virus;
KW neuroprotective; antianaemic; cardiant; cerebroprotective; vulnerary;
KW cytosstatic; immunosuppressive; vitruide; antialcoholic.

OS Spodoptera frugiperda.

XX WO200159108-A2.

XX 16-AUG-2001.

XX 07-FEB-2001; 2001WO-US004071.

XX 10-FEB-2000; 2000US-00502528.

XX (REGC) UNIV CALIFORNIA.

XX (MAED/) MAEDA H.

XX Maeda S, Hammock BD, Huang Q, Maeda H;

XX WPI; 2001-514667/56.
DR N-PSDB; AAD14419.
XX
PT Novel nucleic acid construct comprising cDNA encoding inhibitor of
PT apoptosis proteins, useful for controlling apoptosis in target cells and
PT for combating various disorders associated with apoptosis.
XX
PS Claim 6; Page 39; 43pp; English.

CC The present sequence is fall armyworm inhibitor of apoptosis (IAP). The
CC IAP is useful for controlling apoptosis in target cells. It is also
CC useful for screening compounds that modulate apoptosis and for the
CC production of transgenic plants. The IAP can be used to delay, suppress
CC or inhibit an apoptosis response in plants. In animals, IAPs are used to
CC combat various disorders related to apoptosis, e.g., acquired
CC immunodeficiency syndrome (AIDS), neurodegenerative diseases (e.g.
CC Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis),
CC retinitis pigmentosa and other diseases of retina, myelodysplastic
CC syndrome (e.g., aplastic anaemia), toxin-induced liver diseases (e.g.
CC alcoholism), ischaemic injury (e.g. myocardial infarction, stroke and
CC reperfusion injury), cancers, autoimmune disorders (e.g. lupus
CC erythematosus and multiple sclerosis) and viral infections. The IAP is
CC also useful in vitro to monitor the expression of IAP cDNA, and to detect
CC and monitor the presence of IAPs in a sample. The IAP DNAs are used in
CC the construction of recombinant baculoviruses that are useful as
XX insecticides

SQ Sequence 377 AA;

Query Match 69.5%; Score 1311; DB 4; Length 377;
Best Local Similarity 68.5%; Pred. No. 4.5e-118;
Matches 248; Conservative 39; Mismatches 57; Indels 18; Gaps 7;

QY 1 MELTKVAKNGAAATLVMLKN-ARDAKMRPFIGPLML--SSCESSTSTLPSPSS----- 51
Db 18 MDITKVASNGSSSTLTFKSGSLBAKIRP-LAPLMLPTPSYDSNAGSPSLSPTRCSSSS 76

QY 52 -SADKTDNHDTFNFLPDMRREERLKTFDQWPVTLTPBQLARNGFYLLGRGDEVCC 110
Db 77 FSIDKTDNHDTFGFSADTVDMRKEDERMKTFFKMPVSLSGEQLARNGFYLLGRDEARC 136

QY 111 AFCKVEIMRWEGDDPADHRWAPQCPFVRKQMYANAGGEATAVGRDECGASAA---TQ 167
Db 137 AFCKVEIMRWEGDDPAKDQKRWAPQCPFVRK-LNGTAAADTGSSGQDECGARAAPSGTS 195

QY 168 PPRMPGPVHARYSTEARLATFKDWRMRMRQKPEELAEAGFFYTGQGDKTCKFYCDGGLK 227
Db 196 PPRMAGPVHPRYASEARLRSPKDWPRCMRQKPEELAEAGFFYTGQGDKTCKFYCDGGLK 255

QY 228 DWESDDVPWEQHARWDRCAVQLVGRDYIQVKSEATAISASEEQ--AATNDSTKN 284
Db 256 DWENHDVPWEQHARWDRCAVQLVGRDYIQKISEACEVSASEAERDVAPARTAPSP 315

QY 285 VAQEGEKHLDDSKICKICYSEERNVCFVPGHVAVACAKALSTDKCPMCRRTFTNAVRLY 344
Db 316 PAEAPENSVDSSKLCIKICYAEBERNVCFVPGHVAVACAKALADKCPMCRRTFQNAVRLY 375

QY 345 FS 346
Db 376 FS 377

RESULT 3
ABB09488
ID ABB09488 standard; protein; 263 AA.
XX

XX ABB09488;

XX 01-JUL-2002 (first entry)

XX AMEPV baculovirus-like inhibitor of apoptosis (AMV133).

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: January 6, 2005, 20:01:33 ; Search time 674 Seconds
(without alignments)
6441.806 Million cell updates/sec

Title: US-10-041-859-1

Perfect score: 6692

Sequence: 1 cattacttaaacctcacttcac.....tcgcgcctcactctcgtga 3773

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 3650362

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=UniProt_02 -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bites -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10041859_QCGN 1 1 718 @runat_06012005_133739_3209 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=10 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: UniProt_02:*

1: uniProt_sprot:*\n2: uniProt_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	1887	28.2	346	2	Q968T8
2	1866	27.9	346	2	Q8IS31
3	1333.5	19.9	379	2	Q9U492
4	1319	19.7	377	2	Q9NJ07
5	966	14.4	275	1	IAP_GVCP
6	937	14.0	287	2	Q6E7G7
7	890.5	13.3	280	2	Q6TVV9
8	890.5	13.3	280	2	AAQ91688
9	879	13.1	263	2	Q80SF4
10	876	13.1	281	2	Q9YNL8
11	873	13.0	261	2	Q9QES9
12	873	13.0	276	2	Q89744
13	862	12.9	268	1	IAP3_NPVOP
14	782	11.7	264	2	Q9EN27
15	747.5	11.2	255	2	Q7T5S1
16	728	10.9	289	2	Q7QJ55

17	728	10.9	313	2	Q9J827	Q9J827	spodoptera
18	723.5	10.8	438	1	IAP1_DROME	Q24306	drosophila
19	719.5	10.8	438	2	Q9VUX5	Q9VUX5	drosophila
20	701	10.5	403	2	Q8WRD9	Q8WRD9	aedes trise
21	684	10.2	401	2	Q6Q507	Q6Q507	aedes aegy
22	684	10.2	401	2	AA66751	AA66751	aedes aeg
23	676.5	10.1	402	2	Q8T621	Q8T621	aedes albop
24	662	9.9	285	2	Q8JML6	Q8JML6	mamestra co
25	653	9.8	276	2	Q7IA73	Q7IA73	mamestra co
26	653	9.8	276	2	Q8QL95	Q8QL95	mamestra co
27	653	9.8	276	2	AAQ11158	AAQ11158	mamestra
28	635	9.5	283	2	Q80LK8	Q80LK8	adoxophyes
29	573	8.6	254	2	Q7T9S6	Q7C986	adoxophyes
30	544.5	8.1	269	2	Q6QXJ6	Q6QXJ6	agrotis seg
31	544.5	8.1	269	2	AA882685	AA882685	agrotis s
32	542	8.1	358	1	PIAP_PIG	Q62640	bis scrofa
33	532.5	8.0	268	2	Q9E232	Q9E232	helicoverpa
34	530.5	7.9	401	2	Q8JHV9	Q8JHV9	xenopus lae
35	529.5	7.9	268	2	Q7TLW6	Q7TLW6	helicoverpa
36	529.5	7.9	268	2	Q9IF18	Q9IF18	helicoverpa
37	528.5	7.9	602	2	Q9ESE9	Q9ESE9	rattus norv
38	526.5	7.9	604	1	BIR3_HUMAN	Q13489	homo sapien
39	526	7.9	604	2	Q6DDY3	Q6DDY3	xenopus lae
40	525.5	7.9	600	1	BIR3_MOUSE	Q08863	mus musculu
41	522	7.8	604	2	Q6GLD7	Q6GLD7	xenopus tro
42	516.5	7.7	616	2	Q804E2	Q804E2	ictalurus p
43	514	7.7	647	2	Q8UWD2	Q8UWD2	brachydanio
44	514	7.7	647	2	Q7TOK2	Q7TOK2	brachydanio
45	514	7.7	654	2	Q6ZM93	Q6ZM93	brachydanio

ALIGNMENTS

RESULT 1

Q968T8	PRELIMINARY;	PRT;	346 AA.
ID	Q968T8;		
AC	Q968T8;		
DT	01-DEC-2001 (TREMBLrel. 19, Created)		
DT	01-DEC-2001 (TREMBLrel. 19, last sequence update)		
DT	01-JUN-2003 (TREMBLrel. 24, last annotation update)		
DE	Inhibitor of apoptosis protein.		
GN	Name=IAP;		
OS	Bombyx mori (Silk moth).		
OC	Eukaryota; Metazoa; Archropoda; Hexapoda; Insecta; Pterygota;		
OC	Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;		
OC	Bombycidae; Bombyx.		
OX	NCBI_TaxID=7091;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21240184; PubMed=11341966;		
RA	Huang Q., Deveraux Q.L., Maeda S., Stenicke H.R., Hammock B.D.,		
RA	Reed J.C.;		
RT	"Cloning and characterization of an inhibitor of apoptosis protein		
RT	(IAP) from Bombyx mori."		
RL	Biochim. Biophys. Acta 1499:191-198(2001).		
DR	EMBL; AF281073; AAK57560.1; -.		
DR	HSSP; Q24306; 1JD4.		
DR	GO; GO:0000151; C:ubiquitin ligase complex; IEA.		
DR	GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.		
DR	GO; GO:0008270; F:zinc ion binding; IEA.		
DR	GO; GO:0006916; P:anti-apoptosis; IEA.		
DR	GO; GO:0016567; P:protein ubiquitination; IEA.		
DR	InterPro; IPR001370; BIR.		
DR	InterPro; IPR001841; Znf_ring.		
DR	Pfam; PF00653; BIR; 2.		
DR	SMART; SM00238; BIR; 2.		
DR	SMART; SM00184; RING; 1.		
DR	PROSITE; PS01282; BIR_REPEAT_1; 2.		
DR	PROSITE; PS0143; BIR_REPEAT_2; 2.		
DR	PROSITE; PSS0089; ZF_RING_2; 1.		
DR	SEQUENCE	346 AA; 38942 MW; 6CFC6C6468894C69 CRC64;	

Alignment Scores:

Pred. No.: 2.7e-155 Length: 346
Score: 1887.00 Matches: 346
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 28.20% Indels: 0
DB: 2 Gaps: 0

US-10-041-859-1 (1-3773) x Q968T8 (1-346)

```
QY 206 ATGGAGTTGACGAAGTTGCTAAATAATGAGCTGCCGCCACGTTGGTGTATGTTAAAAAT 265
   |||||||
Db 1 MetGluleuThrIysValAlalysAsnGlyAlaAlaThrIleuValMetLeuIysAsn 20

QY 266 GCGCGGATGCAAAAATGCGACCTTTCATTGGTCCGCTCATGTATCTCTGTTGAGTCT 325
   |||||||
Db 21 AlaArgAspAlaIysMetArgProPheIleGlyProLeuMetLeuSerSerCysGluSer 40

QY 326 TCAACGACATCCACACTCCCGTCACCTTCGTGTCAGCTGATATAAACGGATAATCAGCAG 385
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Db 41 SerThrThrSerThrIleuProSerProSerSerSerAlaAspIysThrAspAsnHisAsp 60

QY 386 ACATTCAACTTCCTTCCTGATATATGCCCGACATGCGTGTGAAGAGAAAGTCTGAAACA 445
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QY 446 TTTGATCAGTGGCCCGTTACGTTTGTGACGCCGGAACAATTGGCCCGCAACGATTCTAC 505
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Db 81 PheAspGlnTrpProValThrPheIeuThrProGluIuLeuAlaArgAsnGlyPheTyr 100

QY 506 TACCTCGTTCGCGCGACGAGAGTGTGCTGTCTTCTGTAAGTAGAATATAGAGTGG 565
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QY 626 CGAAAACAATGTATGCGCAACGCTGGGGAGAGCGCACCGCTGTCCGTAGAGACGAATGT 685
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QY 686 GGGGCCAGTGGCGCCACGACGCTCCCGCATGCCCCGCGCTGACGCGCGTACTCC 745
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Db 161 GlyAlaSerAlaAlaThrGlnProAlaArgMetProGlyProValHisAlaArgTyrSer 180

QY 746 ACCGAGCGCGCGCGCTGCGCACCTTCAAGACTGGCCGAGACGTATGCCCAAAACCC 805
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QY 806 GAGGAATCGCAGAGCGCCGATTCTTCTATACAGGCCCAAGGTGACAAAAGAAATGCTTC 865
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QY 866 TATTGCGACGAGGGCTAAAGAATTGGGAAAGCGATGACGTTCCGTGGGAACAGACGCC 925
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Db 221 TyrCysAspGlyGlyLeuIysAspTyrPglUserAspAspValProTyrGluGlnHisAla 240

QY 926 AGATGTTGACCCGCTGCGCTACGTCGAATTGGTGAAGAAGACGTGACTACATTCAAGAG 985
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QY 986 GTGAAGTCGAGGCCCACTGCGATATCTGCTAGCGAAGAAGAAAGGCCCGCCACCAATGAT 1045
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QY 1046 TCGACTTAAGACGTCGCCCAAGAGGGCGAAGAAACATTGGATGACTTAAATATGTAA 1105
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Db 281 SerThrIysAsnValAlaGlnGluGlyIuIysHisIleuAspAspSerIysIleCysIys 300

QY 1106 ATATGTTATTCGAGGAGCGTAAACGTGTCTTCGTGCGCGTGCACGTTGTCGCGTCC 1165
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QY 1166 GCCAAGTCGCGCGCTGTGACGAGCAAGTCCCGCATGTGTGCGAGACGTTACGAATGCG 1225
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QY 1226 GTGCGCTCTACTTCTCG 1243
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Db 341 ValArgLeuTyrPheSer 346
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RESULT 2
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ID Q8IS31 PRELIMINARY; PRT; 346 AA.
AC Q8IS31;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Inhibitor of apoptosis protein.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_Taxid=7091;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang G., Wang L., Wu X.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY155274; AAN46650.1; -.
DR HSSP; Q24306; 1JD4.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; ZnF_ring.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00238; BIR; 2.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 2.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 346 AA; 38849 MW; 5450EB75F56A8486 CRC64;

Alignment Scores:
Pred. No.: 1.83e-153 Length: 346
Score: 1866.00 Matches: 343
Percent Similarity: 99.13% Conservative: 0
Best Local Similarity: 99.13% Mismatches: 3
Query Match: 27.88% Indels: 0
DB: 2 Gaps: 0

US-10-041-859-1 (1-3773) x Q8IS31 (1-346)

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QY 326 TCAACGACATCCACACTCCCGTCACCTTCGTGTCAGCTGATATAAACGGATAATCAGCAG 385
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QY 386 ACATTCAACTTCCTTCCTGATATATGCCCGACATGCGTGTGAAGAGAAAGTCTGAAACA 445
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QY 446 TTTGATCAGTGGCCCGTTACGTTTGTGACGCCGGAACAATTGGCCCGCAACGATTCTAC 505
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Db 81 PheAspGlnTrpProValThrPheIeuThrProGluIuLeuAlaArgAsnGlyPheTyr 100

QY 506 TACCTCGTTCGCGCGACGAAGTGTGCTGTCTTCTGTAAGTAGAATATAGAGTGG 565
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2005, 18:42:28 ; Search time 10879 Seconds
(without alignments)
12637.844 Million cell updates/sec

Title: US-10-041-859-1
Perfect score: 3773

Sequence: 1 cattacttaactcacttcac.....tcgcgctctactctctcgtga 3773

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	705.6	18.7	712	5	BP121000	BP121000 BP121000
2	685.6	18.2	727	5	BP120885	BP120885 BP120885
3	683	18.1	723	1	AV401669	BP120885 BP120885 AV401669 AV401669
4	649.4	17.2	676	7	CK485834	CK485834 rawb0_00
5	639.8	17.0	658	7	CK505037	CK505037 rawc0_00
6	588.4	15.6	612	7	CK518109	CK518109 rawb0_00
7	577	15.3	624	7	CK564268	CK564268 rawb0_00
8	549.4	14.6	575	7	CK514550	CK514550 rawb0_00
9	546.6	14.5	633	7	CK495885	CK495885 rawb0_00
10	521.4	13.8	622	7	CK497882	CK497882 rawb0_00
11	502.8	13.3	549	7	CK544469	CK544469 rawb0_01
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13	455.8	12.1	555	5	BP121882	BP121882 BP121882
14	453.8	12.0	489	7	CK494236	CK494236 rawb0_00
15	449.6	11.9	459	7	CK500174	CK500174 rawb0_01
16	438.8	11.6	500	5	BP115618	BP115618 rawb0_00
17	428.6	11.4	470	1	AV400060	AV400060 AV400060
18	293.6	7.8	522	7	CK516014	CK516014 rawb0_00
19	179.6	4.8	804	9	CG786123	CG786123 CM_MBa-76
20	121.8	3.2	130	7	CK496041	CK496041 rawb0_00
21	121	3.2	691	4	BM588815	BM588815 170006873
22	114	3.0	712	4	BM601939	BM601939 170006870
23	112.4	3.0	1896	9	CG753083	CG753083 P048-1-C0
24	108.8	2.9	727	7	CF525095	CF525095 AGENCOURT

25	105.6	2.8	592	2	BE978623	BE978623 bee80h08.Y
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28	104	2.8	678	6	CA805412	CA805412 ESG0118a.
29	102.4	2.7	1101	9	CNS00EVL	AL069706 Drosophil
30	102.2	2.7	1539	9	AG340947	AG340947 Mus muscu
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32	102	2.7	636	1	AL872470	AL872470 AL872470
33	102	2.7	644	1	AL854961	AL854961 AL854961
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43	95.6	2.5	1592	9	CG750135	CG750135 P044-3-D0
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45	95.2	2.5	2087	9	AG333887	AG333887 Mus muscu

ALIGNMENTS

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LOCUS BP121000 712 bp mRNA linear EST 16-MAY-2003
DEFINITION BP121000 cen- Bombyx mori cDNA clone cen-4016, mRNA sequence.
ACCESSION BP121000
VERSION BP121000.1 GI:29554042
KEYWORDS EST.
SOURCE Bombyx mori (domestic silkworm)
ORGANISM Bombyx mori

REFERENCE
AUTHORS Mita,K., Morimyo,M., Shimada,T., Okano,K. and Maeda,S.
TITLE Bombyx mori cDNA (Mita,K. 2003)
JOURNAL Unpublished (2003)
COMMENT Contact: Mita K
Genome Research Group
National Institute of Agrobiological Sciences
Owashi 1-2, Tsukuba, Ibaraki 305-8634, Japan
Email: kmita@nias.affrc.go.jp
method:uni-directional, sequence direction:sequenced from T3 primer
(5' -> 3').

FEATURES
source

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Matches 708; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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 QY 1265 CTGTACTACTAATCACTTCACCGGGCGGCTGAGCGTGTGAACCACTTCGAACGA 1324
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 ACCESSION BP120885
 VERSION BP120885.1 GI:29553920
 KEYWORDS EST.
 SOURCE Bombyx mori (domestic silkworm)
 ORGANISM Bombyx mori
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea; Bombycidae; Bombyx.
 1 (bases 1 to 727)
 Mita,K., Morimyo,M., Shimada,T., Okano,K. and Maeda,S.
 TITLE Bombyx mori cDNA (Mita,K. 2003)
 JOURNAL Unpublished (2003)
 COMMENT Contact: Mita K
 Genome Research Group
 National Institute of Agrobiological Sciences
 Owashi 1-2, Tsukuba, Ibaraki 305-8634, Japan
 Email: kmita@nias.affrc.go.jp
 method:uni-directional, sequence direction:sequenced from T3 primer (5' -> 3').

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 QY 725 CCGGTGACCGCGGCTACTCCACCGAGCGCGCGGCTTGGCCACTTCAAGACTGGCGG 784
 Db 61 CCGGTGACCGCGGCTACTCCACCGAGCGCGCGGCTTGGCCACTTCAAGACTGGCGG 120
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 Db 181 GGTGACAAAACGAAATGCTTCTATTTGCGACGAGGGCTAAAAGATTGGAAAGCGATGAC 240
 QY 905 GTTCCGTGGGAACAGACGCCAGATGGTTCGACCGCTGCGCGTACGTAATTTGGTAAA 964
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 Db 361 GAACAGCGCCGACCAATGATTCGACTAAGACGTGCCCTCAAGAGGGCGAAGAACATTTG 420
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RESULT 3
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 VERSION AV401669
 KEYWORDS AV401669.1 GI:6905321
 SOURCE EST.
 ORGANISM Bombyx mori (domestic silkworm)
 Bombyx mori
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea; Bombycidae; Bombyx.
 1 (bases 1 to 723)
 Mita,K., Morimyo,M., Shimada,T., Okano,K. and Maeda,S.

Db 41 ValArgCysAlaPheCysValGluIleMetArgTrpLysGluGlyLysAspProAla 60
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 Db 61 AlaAspHisLysLysTrpAlaProGlnCysProPheValLys----- 74
 QY 647 GCTGGGGAGAGGCGCGCTGTCGGTAGAGACCAATGTGGGGCCAGTCCGCCACGAG 706
 Db 75 -----GlyIleAspValCysGlySerIleValThrThrAsn 86
 QY 707 -----CCTCCCGCATGCCCGGCCCGCGTGCACCGCGGTACTCC 745
 Db 87 AsnIleGlnAsnThrThrHisAspThrIleIleGlyProAlaHisProLysTyrAla 106
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 C;Accession: T10304
 R;Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohmann, G.F.
 Virology 229, 381-399, 1997
 A;Title: The sequence of the Orygia pseudotsugata multinucleocapsid nuclear polyhedrosis
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Query Match: 12.88% Indels: 22
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 QY 713 CGCATGCCCGCGCCCGTGCACGCGCGGTACTCCACGAGCGCGCGGCTCGCCACCTTC 772
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 Db 119 AlaGluTrpProArgGlyLeuLysGlnArgProGlnGluLeuAlaGluAlaGlyPhePhe 138
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 QY 1073 GAGAAACATTTGATGACTCTAAATATGTAAATATGTTATTCGAGAGCGTAACTG 1132
 Db 212 GluAlaGluValAlaAspAspArgLeuCysLysIleCysLeuGlyAlaGluLysThrVal 231
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 C;Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 09-Jul-2004
 C;Accession: A53989
 R;Birnbau, M.J.; Clem, R.J.; Miller, L.K.
 J. Virol. 68, 2521-2528, 1994
 A;Title: An apoptosis-inhibiting gene from a nuclear polyhedrosis virus encoding a polyp
 A;Reference number: A53989; MUID:94187094; PMID:8139034
 A;Accession: A53989
 A;Status: preliminary

GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	109.8	2.9	8056	US-10-473-126-386	Sequence 386, App
4	104	2.8	1317	US-10-267-502-202	Sequence 202, App
5	99.8	2.6	3673778	US-10-312-841-2	Sequence 2, Appli
6	95.6	2.5	8056	US-10-473-126-240	Sequence 240, App
7	94.6	2.5	5979	US-10-239-676-18	Sequence 18, Appli
8	94.6	2.5	5979	US-10-240-453-26	Sequence 26, Appli
9	94.2	2.5	8056	US-10-473-126-240	Sequence 240, App
10	93.2	2.5	74665	US-10-719-993-6854	Sequence 6854, App
11	91.8	2.4	843	US-10-244-586-2	Sequence 2, Appli
12	91.8	2.4	1068	US-10-203-708-21	Sequence 21, Appli

13	91.8	2.4	1168	16	US-10-188-646-12	Sequence 12, Appli
14	91.8	2.4	1260	16	US-10-188-646-4	Sequence 4, Appli
15	91.8	2.4	1268	18	US-10-807-897-28	Sequence 28, Appli
16	91.8	2.4	1322	18	US-10-807-897-26	Sequence 26, Appli
17	91.8	2.4	1337	14	US-10-235-026-1	Sequence 1, Appli
18	91.8	2.4	1363	18	US-10-839-883-37	Sequence 37, Appli
19	91.8	2.4	1376	14	US-10-244-586-1	Sequence 1, Appli
20	88.2	2.3	5979	14	US-10-239-676-18	Sequence 18, Appli
21	88.2	2.3	5979	15	US-10-240-453-26	Sequence 26, Appli
22	87.8	2.3	635	10	US-09-991-936-1622	Sequence 1622, Ap
23	86.6	2.3	3673778	15	US-10-312-841-1	Sequence 1, Appli
24	85.2	2.3	3673778	15	US-10-312-841-1	Sequence 1, Appli
25	81	2.1	769	15	US-10-203-708-22	Sequence 22, Appli
26	78	2.1	615	16	US-10-296-115-63	Sequence 63, Appli
27	77.8	2.1	14919	16	US-10-221-714A-228	Sequence 228, Appli
28	77.4	2.1	5611	17	US-10-433-793-100	Sequence 100, App
29	77	2.0	16217	15	US-10-311-455-597	Sequence 597, App
30	76.8	2.0	15548	15	US-10-311-455-2128	Sequence 2128, Ap
31	75.8	2.0	15373	15	US-10-311-455-439	Sequence 439, App
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34	75.2	2.0	13574	15	US-10-311-455-1290	Sequence 1290, Ap
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ALIGNMENTS

RESULT 1
US-10-041-859-1
; Sequence 1, Application US/10041859
; Publication No. US20030049796A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, QIHONG
; APPLICANT: REED, JOHN C.
; APPLICANT: DEVERAUX, QUINN L.
; APPLICANT: MAEDA, SUSUMU
; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND
; TITLE OF INVENTION: METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 087102/027 2537
; CURRENT APPLICATION NUMBER: US/10/041, 859
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260, 478
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3773
; TYPE: DNA
; ORGANISM: Bombyx mori
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2733)..(3770)
; US-10-041-859-1

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Perfect score: 3773

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SUMMARIES

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16	74	2.0	2563	4 US-09-016-434-1076	Sequence 1076, Ap
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ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/09502528
; Patent No. 6570069
; GENERAL INFORMATION:
; APPLICANT: Hammock, Bruce D.
; APPLICANT: Huang, Qihong
; APPLICANT: Maeda, Susumu
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Inhibitors of Apoptosis
; FILE REFERENCE: 023070-112000US
; CURRENT APPLICATION NUMBER: US/09/502, 528
; CURRENT FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1739
; TYPE: DNA
; ORGANISM: Spodoptera frugiperda
; FEATURE:
; OTHER INFORMATION: fall armyworm inhibitor of apoptosis protein
; OTHER INFORMATION: (SFIAP) nucleotide sequence including 5' and 3'
; OTHER INFORMATION: untranslated regions, full length SFIAP cDNA
; NAME/KEY: CDS
; LOCATION: (229)..(1362)
; OTHER INFORMATION: fall armyworm inhibitor of apoptosis protein
; OTHER INFORMATION: (SFIAP)
US-09-502-528-1

Query Match	11.7%;	Score 441.8;	DB 4;	Length 1739;
Best Local Similarity	69.7%;	Pred. No. 1.2e-95;		
Matches 650;	Conservative 0;	Mismatches 262;	Indels 21;	Gaps 3;
QY	343	CCCCGCACCTTCGTCGCTGACGTGATAAACGGATATCAACGACACATTCACCTTCCTCC	402	
Db	444	CTCTTCATCTTCTTCTTCATGTATAAACCGACCAACGACACCTTCGGCTTCAGTGC	503	
QY	403	TGATATGCCCGACATGCGTCGTGAAGAGGAACGCTGAAAAACATTGATCAGTGGCCGT	462	
Db	504	GGACACAGTTGATATGAGAAAAGAGATGAACGTATGAAAAACATTGAAAAATGGCCGT	563	
QY	463	TACGTTTGTGACGCGGACAAATTTGCCCGAACGATTTCTACTACCTCGTGGCGCGA	522	
Db	564	AAGTTTTCATCCGAGACCAACTGCTCGAAATGATTTTACTACCTCGGCCGTAGAGA	623	
QY	523	CGAAGTGTGCTGTGCTTCTGTAGGTAAGGTAAGAAATTATGAGGTGGTGAAGCGAGATCC	582	
Db	624	TGAAGCCCGTGGCGCTTCTGTAAAGTGAGATTAATGAGGTGGTGAAGCGCGATGACC	683	
QY	583	TGCCCGCGATCATCGAGATGGGCGCCCGCAGTGTCCCTTTGTACGAAAAACAATGTATGC	642	

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Db      684  TCGGAAGGACCATCAGCGTTGGGCGCCACAGTGCCTATTTGTGCGCA---AATTGAACGG 740
QY      643  CAACGCTGGGGGAGAGGCGCAGCCGTGTGCTGAGAGCAATGTGGGCCAGTGGCGC--- 699
Db      741  TACTGCAGCAGACAGACCGGTAAGTTCGGGCCAGAGCAGTGTGTGCCCCGCGCGCTCC 800
QY      700  -----CAGCGAGCCTCCCGCATGCGCCCGCGCGCGCGCGCGCGCTACTCCACGAGGC 753
Db      801  CTCGGTAACCTCTCCGCGCGTATGCGCGGTCCCGTGCACCCACGATATGATCTGAAGC 860
QY      754  CGCGCGGCTCGCCACCTTCAAGGACTGGCCGAGACGTAAGCCCAAAAACCCGAGAACT 813
Db      861  CGCAGCACTACGCACTTTAAAGACTGGCCACGATGATGCGACAAAACCTGAAGAACT 920
QY      814  GCGAGAGCGCGGATTTCTTCTATACAGGCCAAGGTGACAAAACGAAATGCTTCTATTGCCA 873
Db      921  CGCCGAGGCTGGCTTTTTCACACTGCTCAGGGAACAAAACCAAGTGTTTTATTGCCA 980
QY      874  CGAGAGGCTAAAGATTGGGAAAGCGATGACGTTCCGTGGGAAACAGCAGCCGATGGTT 933
Db      981  TGGTGGATTAAAGATTGGGAAACCATGACGTAACCTGGGAAACACACGCAAGGTGTT 1040
QY      934  CGACCGCTGCGCGTACGTCGAATTGGTAAAGAGCGTGAATTCATTGAGAGGTGAAGTC 993
Db      1041  TGACCGTTCGCGCTACGTCGAATTGGTAAAGGTGAGAAATACGTTCAAAAGGTGATTTTC 1100
QY      994  GAGAGGCTGCGGATATCTGCTAGCGAAGAAAGAGG-----CCGCCACCAATGA 1044
Db      1101  TGAAGCTTGTAGGATATCCGCTCAGAAAGCGAAGTATGACACCCGACGCACTGC 1160
QY      1045  TTGCACTAAGAACGTGCGCCCAAGAGGCGGAGAAACATTTGATGACTTAAATATGTAA 1104
Db      1161  CGAGCCAAAGCCCGCAGAGAGGCGCCAGAAAACCTCAGTCACTCAAGTGTGTAA 1220
QY      1105  AATATGTTATTCGAGAGCGTAAAGTGTGCTTGTGCGCGCGGCGGAGTGTGGCGTG 1164
Db      1221  AATCTGTTATCTGAAGAGCGTAAAGTGTGCTTGTGCGCGCGGCGGAGTGTGGCGTG 1280
QY      1165  CGCCAAGTGGCGCTGTGACGAGCAAGTGCCTGATGTGCGAGACGTTCAAGATGC 1224
Db      1281  CGCCAAGTGGCGCTGTGCGCGCGCGCGCAGCAAGTGCCTGCGCAGGACGTTTCAAAATGC 1340
QY      1225  GGTGCGGCTCTACTTCTCGTGAAGAGACCCTCC 1257
Db      1341  AGTGGCGTATATTTCTCGTGAAGAGACCACC 1373

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RESULT 2
US-09-502-528-2
; Sequence 2, Application US/09502528
; Patent No. 6570069
; GENERAL INFORMATION:
; APPLICANT: Hammock, Bruce D.
; APPLICANT: Huang, Qihong
; APPLICANT: Maeda, Susumu
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Inhibitors of Apoptosis
; FILE REFERENCE: 023070-112000US
; CURRENT APPLICATION NUMBER: US/09/502,528
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1134
; TYPE: DNA
; ORGANISM: Spodoptera frugiperda
; FEATURE:
; OTHER INFORMATION: Sf1AP nucleotide sequence, open reading frame
; NAME/KEY: CDS
; LOCATION: (1)..(1134)
; OTHER INFORMATION: fall armyworm inhibitor of apoptosis protein

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OTHER INFORMATION: (SFIAP)
US-09-502-528-2

Query Match 11.6%; Score 437.2; DB 4; Length 1134;
Best Local Similarity 69.7%; Pred. No. 1.2e-94;
Matches 643; Conservative 0; Mismatches 258; Indels 21; Gaps 3;

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QY      343  CCCGTCACCTTTCGTCGTCAGCTGATTAACCGATAATCACGACATTCACCTTCTTCC 402
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QY      523  CGAAGTGTCTGTGCTTCTGTAAAGTAAATAATTATGAGTGGGTGGAAGCGCATCC 582
Db      396  TGAAGCCCGTTCGCTTCTGTAAAGTGAAGATTATGAGTGGGTGAGGCGCATGACCC 455
QY      583  TGCCGCGGATCATCGGAGATGGGCGCCCAAGTGTCCCTTTGTAAGAAAACAAATGTATGC 642
Db      456  TCGAAGGACCATCAGCGTGTGGGCGCCACAGTGCCTATTTGTGCGCA---AATTGAACGG 512
QY      643  CAACGCTGGGGGAGAGGCGACCGCTGCTGTAAGACGAATGTGGGCCAGTGGCGC--- 699
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QY      700  -----CAGCAGCCTCCCGCATGCGCGCGCGCGCGCGCGCGTACTCCACCGAGGC 753
Db      573  CTCGGTAACCTCTCCGCGCGTATGCGCGGTCCCGTGCACCCACGATATGATCTGAAGC 632
QY      754  CGCGGCGCTCGCCACCTTCAAGAGCTGGCCGAGACGTAAGCCCAAAAACCCGAGAACT 813
Db      633  CGCAGCACTACGCACTTTTAAAGACTGGCCACGATGCAATGCAAAAACCTGAAGAACT 692
QY      814  GGCAGAGGCGCGATTTCTTCTATACAGGCCAAGGTGACAAAACGAAATGCTTCTATTGCCA 873
Db      693  CGCGAGGCTGGCTTTTTCACACTGCTGTCAGGAGAGCAAAAACCAAGTGTTTTATGCCA 752
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Db      753  TGGTGGATTAAAGATTGGGAAACCATGACGTAACCTGGGAAACACACGCAAGGTGTT 812
QY      934  CGACCGCTGCGCGTACGTCGAATTGGTAAAGAGCGTGAATTCAGATTCAGAAAGTGAAGTC 993
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QY      994  GAGAGGCTGCGGATATCTGCTAGCGAAGAAAGACAGG-----CCGCCACCAATGA 1044
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QY      1045  TTGCACTAAGAACGTGCGCCCAAGAGGCGGAGAAACATTTGATGACTTAAATATGTAA 1104
Db      933  CGAGCCAAAGCCCGCAGAGAGGCGCCAGAAAACCTCAGTCACTCAAGTGTGTAA 992
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QY      1165  CGCCAAGTGGCGCTGTGACGAGCAAGTGCCTGATGTGCGAGACGTTCAAGATGC 1224
Db      1053  CGCCAAGTGGCGCTGTGCGCGCGCGCAGCAAGTGCCTGCGCAGGACGTTTCAAAATGC 1112
QY      1225  GGTGCGGCTCTACTTCTCGTGA 1246
Db      1113  AGTGGCGTATATTTCTCGTGA 1134

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RESULT 3

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2005, 16:43:28 ; Search time 1653 Seconds
(without alignments)
11981.891 Million cell updates/sec

Title: US-10-041-859-1

Perfect score: 3773

Sequence: 1 cattatcaactcacttcac.....tgcggctctactctcgtga 3773

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 1: geneseqn1980a:*
- 2: geneseqn1990a:*
- 3: geneseqn2000a:*
- 4: geneseqn2001a:*
- 5: geneseqn2001b:*
- 6: geneseqn2002a:*
- 7: geneseqn2002b:*
- 8: geneseqn2003a:*
- 9: geneseqn2003b:*
- 10: geneseqn2003c:*
- 11: geneseqn2003d:*
- 12: geneseqn2004a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3773	100.0	3773	6 ABQ78228	Abq78228 Nucleotid
2	441.8	11.7	1739	5 AAD14419	Aad14419 Fall army
C 3	142.4	3.8	50000	6 ABL55643	Ab155643 AMEPV gen
4	130.4	3.5	794	6 ABL55635	Ab155635 AMEPV bac
C 5	111.8	3.0	8056	8 ABZ10246	Abz10246 Haematopo
6	109.8	2.9	8056	8 ABZ10246	Abz10246 Haematopo
7	105.6	2.8	1304	5 AAC84527	Aac84527 Drosophil
8	105.6	2.8	1317	5 AAC84520	Aac84520 Drosophil
9	105.6	2.8	1317	5 AAC84529	Aac84529 Drosophil
10	105.6	2.8	1317	5 AAC84521	Aac84521 Drosophil
11	105.6	2.8	1317	5 AAC84525	Aac84525 Drosophil
12	105.6	2.8	1317	5 AAC84522	Aac84522 Drosophil
13	105.6	2.8	1317	5 AAC84526	Aac84526 Drosophil
14	105.6	2.8	1317	5 AAC84528	Aac84528 Drosophil
15	105.6	2.8	1317	5 AAC84524	Aac84524 Drosophil
16	104	2.8	1317	5 AAC84523	Aac84523 Drosophil
17	104	2.8	1317	12 ADO07876	Ado07876 Fly polyn
18	104	2.8	1858	4 ABL21061	Ab121061 Drosophil
19	104	2.8	2013	4 ABL10083	Ab110083 Drosophil
20	104	2.8	10432	4 ABL10082	Ab110082 Drosophil
21	104	2.8	14250	4 ABL21060	Ab121060 Drosophil

C 22	95.6	2.5	8056	8 ABZ10100	Abz10100 Haematopo
C 23	94.6	2.5	5979	4 AAS45313	Aas45313 Chemical1
C 24	94.6	2.5	5979	6 ABK28152	Abk28152 DNA trans
C 25	94.2	2.5	8056	8 ABZ10100	Abz10100 Haematopo
26	91.8	2.4	672	6 AAL42857	Aal42857 Survivin-
27	91.8	2.4	723	6 AAL42856	Aal42856 Survivin-
28	91.8	2.4	840	6 AAL42858	Aal42858 Survivin-
29	91.8	2.4	843	4 AAF24857	Aaf24857 Nucleotid
30	91.8	2.4	1068	4 AAD16364	Aad16364 Human SBh
31	91.8	2.4	1168	12 ADH89543	Adh89543 Human Liv
32	91.8	2.4	1260	12 ADH89535	Adh89535 Human Liv
33	91.8	2.4	1268	10 ACC72844	Acc72844 Human can
34	91.8	2.4	1322	10 ACC72843	Acc72843 Human can
35	91.8	2.4	1337	3 AAZ61210	Aaz61210 DNA encod
36	91.8	2.4	1363	3 AAA15007	Aaa15007 CDNA enco
37	91.8	2.4	1376	4 AAF24856	Aaf24856 Nucleotid
C 38	90.4	2.4	131680	10 ADF29092	Adf29092 Agrotis s
39	88.2	2.3	5979	4 AAS45313	Aas45313 Chemical1
40	88.2	2.3	5979	6 ABK28152	Abk28152 DNA trans
41	87.8	2.3	635	3 AAC95127	Aac95127 Cat flea
C 42	82	2.2	8310	2 AAZ29911	Aaz29911 CDNA enco
43	81	2.1	769	4 AAD16365	Aad16365 Human SBh
44	78.6	2.1	204	6 AAL42854	Aal42854 Survivin-
45	78	2.1	614	5 AAS91550	Aas91550 DNA encod

ALIGNMENTS

RESULT 1	ABQ78228	standard; cDNA; 3773 BP.
ID	ABQ78228	
XX		
AC	ABQ78228;	
XX		
DT	22-OCT-2002	(first entry)
XX		
DE	Nucleotide sequence of inhibitor of apoptosis protein BmiAP.	
XX		
KW	Inhibitor of apoptosis protein; IAP; BmiAP; silkworm; apoptosis; insect;	
KW	Spodoptera frugiperda; insul-resistant plant; caspase; gene; ss.	
XX		
OS	Bombyx mori.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	2733..3773
FT		/*tag= a
FT		/product= "inhibitor of apoptosis protein BmiAP"
XX		
PN	WO200253586-A2.	
XX		
PD	11-JUL-2002.	
XX		
PF	07-JAN-2002; 2002WO-US000314.	
XX		
PR	08-JAN-2001; 2001US-0260478P.	
XX		
PA	(BURN-) BURNHAM INST.	
XX		
PI	Maeda S, Huang Q, Reed JC, Deveraux QL;	
XX		
DR	WPI; 2002-590628/63.	
DR	P-PSDB; ABB78046.	
XX		
PT	Novel recombinant polypeptide, inhibitor of apoptosis protein family	
PT	member BmiAP from silkworm Bombyx mori BmN cells, useful for inhibiting	
PT	apoptosis and identifying an agent that modulates activity of	
PT	polypeptide.	
XX		
PS	Claim 8; Page 29-30; 62pp; English.	
XX		
CC	The present score encodes a polypeptide which is an inhibitor of	
CC	apoptosis protein (IAP) family member, and designated BmiAP. BmiAP is	

CC derived from silkworm *Bombyx mori* BmN cells. The BmIAP polypeptide
CC contains two baculoviral IAP repeat (BIR) domains, followed by a RING
CC domain. BmIAP polypeptides and polynucleotides are useful for inhibiting
CC apoptosis in insect cells, especially *Spodoptera frugiperda* or *Bombyx*
CC *mori* cells, and mammalian cells, and plant cells. They are also useful
CC for generating a biotic or abiotic insulin-resistant plant. BmIAP is also
CC useful for inhibiting caspases

5Q Sequence 3773 BP; 1108 A; 785 C; 866 G; 1014 T; 0 U; 0 Other;

Query Match	100.0%;	Score 3773;	DB 6;	length 3773;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 3773; Conservative	0;	Mismatches	0;	Indels 0;
				Gaps 0;

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QY 121 TTCTTGCAAGACGAGTGTCACTGATTTAAACAAAAACATAAGATAGACGTTTATGCGTT 180
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Db 121 TTCTTGCAAGACGAGTGTCACTGATTTAAACAAAAACATAAGATAGACGTTTATGCGTT 180
|||||

QY 181 ACTAAAAAAAAATATACCAATGAGTTGACGAAGTTGCTAAAAAATGAGCTGC 240
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Db 181 ACTAAAAAAAAAGGAAAATAATACCAATGAGTTGACGAAGTTGCTAAAAAATGAGCTGC 240

[illegible][illegible]

Dy 361 AGCTGATAAAACGGATTAATCAGACACATTCACTTCTCGATATGCCGCATGGC 420
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Db 361 AGCTGATAAAACGGATTAATCAGACACATTCACTTCTCGATATGCCGCATGGC 420

OY 421 TCGTGAAGAGGACGTCTGAAAACATTTGATCAGTGGCCCGTTACGTTTTTGACGCCCGA 480
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 421 TCGTGAAGAGGACGTCTGAAAACATTTGATCAGTGGCCCGTTACGTTTTTGACGCCCGA 480

[illegible][illegible]

QY 601 ATGGGCGCCAGTGTCCCTTTGTACGAACAATGTATGCCACGCTGGGGGAGAGGC 660
|||||
Db 601 ATGGGCGCCAGTGTCCCTTTGTACGAACAATGTATGCCACGCTGGGGGAGAGGC 660
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QY 661 GACCGCTGTGGTAGAGACGAATGTGGGGCCAGTGGGGCCACGCAGCCTTCCCCGCATGCC 720
|||||
Db 661 GACCGCTGTGGTAGAGACGAATGTGGGGCCAGTGGGGCCACGCAGCCTTCCCCGCATGCC 720
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QY	721	CGGCCCCGTGCACGCGCGGTACTCCACCGAGGCCGCGGCTCGCCACTTCAAGGACTG	780
Db	721	CGGCCCCGTGCACGCGCGGTACTCCACCGAGGCCGCGGCTCGCCACTTCAAGGACTG	780

QY 781 GCCGAGACGTATGCCCAAAAACCCGAGAACTGGCAGAGGCCGATTTCTTATACAGG 840
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|||

OY 841 CCAAGGTGACAAAACGAATGCTTCTATTGCCGACGGAGGGCTAAAGAATTGGGAAAGCGA 900
|||||
D6 841 CCAAGGTGACAAAACGAATGCTTCTATTGCCGACGGAGGGCTAAAGAATTGGGAAAGCGA 900
|||||

QY 901 TGACGTTCCGTGGGAACAGCAGCCAGATGTTTCGACCGCTGCGCGTACGTGCAATGGT 960

QY 961 GAAAGACGTGACTACATTCAGAGGTGAAGTCGAGGCCACTCGATATCTGTAACGA 1020

QY 1021 AGAGACAAGGCCGCCACCAATGATTGACTAAGAACGTGCCCCAAGAGGGCGGAAACA 1080

	TTTGATGACTTAATAATATGTAAATATGTATTCCGAGGAGCGTAAACGTGTCTTCGT	1140
QY		

1141 GCCGTGCGGCCACCGTGGTGGCTGCGCCAAAGTGGCGCTGTGACGAGCAAGTGGCCGAT 1200

1201 GTGTGGCAGGACGTTACGAATGCGGTGCGGCTACTTCTCGTGAAAGACCTCTCG 1260

1261 CGAGCTGTACTAATCACTTCACCGGGCGCGCTTGAGCGTGTGAACCACTTCGA 1320

QY 1321 ACGAAACCGCGTATCTGTGATTTTACATTAATAATTACAAATGATAGCGGTGG 1380

1381 GCAATGTATAGAACTCGTCAGAACTCGCGAGTTGACGTGCAGAGAGATTAGTGATTT 1440

1441 GTAACTTGTAACTGATGTTGAATGATTTATTATTATTAAATTTCTAATGACAAA 1500

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QY 1741 GATTCACTTCCCTGTGTAAGTGATAAAATTCTATGTAAATCCAGAGTTTAAATGTCG 1800

D8 1741 G A I I C A C I I C C C C I G T G A A G I G A Y A A A A T C T A A T G A A M I C A G A G T T A A A T G T C G 1800

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1801 TCAAAATTAATTAAGAACACAGTTTACGCTTCTTTTGGTTGAAAAATCTATAATTGA 1860
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1921 TATGATTAATTCGACATAATTATGGCAATTCGTAAGATACATCCATACCTATT 1980

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: January 6, 2005, 19:57:18 ; Search time 443 Seconds
(without alignments)
6141.921 Million cell1 updates/sec

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1603904 seqs, 360571292 residues

Total number of hits satisfying chosen parameters: 3207808

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Published Applications_AA:*

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- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result * Query

No.	Score	Match	Length	DB	ID	Description
1	1887	28.2	346	14	US-10-041-859-2	Sequence 2, Appli
2	966	14.4	275	9	US-09-201-936-12	Sequence 12, Appli
3	966	14.4	275	14	US-10-323-643-9	Sequence 9, Appli
4	966	14.4	275	16	US-10-600-272-12	Sequence 12, Appli
5	932.5	13.9	172	14	US-10-041-859-8	Sequence 8, Appli
6	862	12.9	268	14	US-10-323-643-10	Sequence 10, Appli
7	846.5	12.6	172	14	US-10-041-859-10	Sequence 10, Appli
8	831.5	12.4	172	14	US-10-041-859-9	Sequence 9, Appli
9	759.5	11.3	172	14	US-10-041-859-11	Sequence 11, Appli
10	719.5	10.8	438	15	US-10-267-502-419	Sequence 419, App
11	696.5	10.4	172	14	US-10-041-859-12	Sequence 12, Appli
12	554.5	8.3	172	14	US-10-041-859-13	Sequence 13, Appli
13	526.5	7.9	604	14	US-10-232-286-4	Sequence 4, Appli
14	526.5	7.9	604	14	US-10-141-618-6	Sequence 6, Appli
15	526.5	7.9	604	14	US-10-366-307-6	Sequence 6, Appli
16	526.5	7.9	604	16	US-10-730-476A-79	Sequence 79, Appli
17	526.5	7.9	604	17	US-10-825-282-40	Sequence 40, Appli
18	525.5	7.9	600	9	US-09-974-592-12	Sequence 12, Appli
19	525.5	7.9	600	17	US-10-482-952-1	Sequence 1, Appli
20	524.5	7.8	604	9	US-09-974-592-6	Sequence 6, Appli
21	524.5	7.8	604	9	US-09-201-936-6	Sequence 6, Appli
22	524.5	7.8	604	16	US-10-636-065-221	Sequence 221, App
23	524.5	7.8	604	16	US-10-600-272-6	Sequence 6, Appli
24	517.5	7.7	602	9	US-09-201-936-40	Sequence 40, Appli
25	517.5	7.7	602	16	US-10-636-065-227	Sequence 227, App
26	517.5	7.7	602	16	US-10-600-272-40	Sequence 40, Appli
27	507.5	7.6	618	9	US-09-974-592-8	Sequence 8, Appli
28	507.5	7.6	618	9	US-09-201-936-8	Sequence 8, Appli
29	507.5	7.6	618	16	US-10-636-065-223	Sequence 223, App
30	507.5	7.6	618	16	US-10-600-272-8	Sequence 8, Appli
31	500.5	7.5	498	9	US-09-201-936-13	Sequence 13, Appli
32	500.5	7.5	498	16	US-10-600-272-13	Sequence 13, Appli
33	500.5	7.5	618	14	US-10-153-668-338	Sequence 338, App
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36	500.5	7.5	618	14	US-10-366-307-4	Sequence 4, Appli
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38	500.5	7.5	618	15	US-10-260-708-63	Sequence 63, Appli
39	500.5	7.5	618	16	US-10-476A-78	Sequence 78, Appli
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42	497.5	7.4	497	9	US-09-974-592-4	Sequence 4, Appli
43	497.5	7.4	497	9	US-09-201-936-4	Sequence 4, Appli
44	497.5	7.4	497	16	US-10-636-065-219	Sequence 219, App
45	497.5	7.4	497	16	US-10-600-272-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-10-041-859-2
; Sequence 2, Application US/10041859
; Publication No. US20030049796A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, QIHONG
; APPLICANT: REED, JOHN C.
; APPLICANT: MAEDA, SUSUMU
; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND
; TITLE OF INVENTION: METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 087102/027 2537
; CURRENT APPLICATION NUMBER: US/10/041, 859
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260, 478
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Bombyx mori

US-10-041-859-2

Alignment Scores:

Pred. No.: 4.13e-166
Score: 1887.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 28.20%
DB: 14
Length: 346
Matches: 346
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-10-041-859-1 (1-3773) x US-10-041-859-2 (1-346)

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QY 266 GCGCGGGATGCAAAAATGCGACCTTTCATTGGTCGGCTCATGTTATCTCTGTGAGTCT 325
Db 21 AlaArgAspAlaIysMetArgProPheIleGlyProLeuMetLeuSerSerCysGluSer 40
QY 326 TCAACGACATCCAGACTCCCGTCACCTTCGTCGCTCAGCTGATATAAACGGATTAATCAGCAG 385
Db 41 SerThrThrSerThrLeuProSerProSerSerSerAlaAspLysThrAspAsnHisAsp 60
QY 386 ACATTCAACTTCCTTCCTGATATATGCCCGACATGCGTCGTGAAGAGGAACGTCTGAAACA 445
Db 61 ThrPheAsnPheLeuProAspMetProAspMetArgArgGluGluGluValGlyLeuLysThr 80
QY 446 TTTGATCAGTGGCCCGTTACGTTTGTGACGCCCGGAACAATTTGGCCCGCAACGATTTCTAC 505
Db 81 PheAspGlnTrpProValThrPheLeuThrProGluGlnLeuAlaArgAsnGlyPheLysThr 100
QY 506 TACCTCGGTCCGGCGGACGAAGTGTGCTGCTTCTGTAAAGGTAGAAATTATGAGGTGG 565
Db 101 TyrLeuGlyArgGlyAspGlyValCysCysAlaPheCysLysValGluIleMetArgTrp 120
QY 566 GTCGAAGCGCAGCATCTCTGCCCGCGATCATCGAGATGGCGCCCGCCAGTGTCCCTTTGTA 625
Db 121 ValGluGlyAspAspProAlaAlaAspHisArgArgTrpAlaProGlnCysProPheVal 140
QY 626 CGAAAACAATGTATGCAACGCTGGGGGAGCGACCGCTGTGGTAGAGCAATGT 685
Db 141 ArgLysGlnMetTyrAlaAsnAlaGlyGlyGluAlaThrAlaValGlyArgAspGluCys 160
QY 686 GGGCCAGTGGCGCCACGACGCTCCCGCGATGCCCGCGCCCGCGCTGACCGCGGTACTCC 745
Db 161 GlyAlaSerAlaAlaThrGlnProProArgMetProGlyProValHisAlaArgTyrSer 180
QY 746 ACCGAGCGCGCGCTGCCACCTTCAAGACTGGCCGAGACGTATGCGCCCAAAACC 805
Db 181 ThrGluAlaAlaArgLeuAlaThrPheLysAspTrpProArgArgMetArgGlnLysPro 200
QY 806 GAGGAATGGCAGAGCGCGGATTTCTTATACAGGCCCAAGGTGACAAAACGAATGCTTC 865
Db 201 GluGluLeuAlaGluAlaGlyPhePheTyrThrGlyGlnGlyAspLysThrLysCysPhe 220
QY 866 TATTGCGACGAGGGCTAAAGATTGGGAAAGCATGACGTTCCGTGGGAAACAGACGCGC 925
Db 221 TyrCysAspGlyGlyLeuLysAspTrpGlnSerAspAspValProTrpGluGlnHisAla 240
QY 926 AGATGTTGACCGCTGCGCGTACGTAATGTTGTAAGAGAGACGTAATACATTCAAGAG 985
Db 241 ArgTrpPheAspArgCysAlaTyrValGlnLeuValLysGlyArgAspTyrIleGlnLys 260
QY 986 GTGAAGTCGAGGCCACTGCGATATCTGCTAGCGAAGAGAGACAGCGCCACCAATGAT 1045
Db 261 ValLysSerGluAlaThrAlaIleSerAlaSerGluGluGluGlnAlaAlaThrAsnAsp 280
QY 1046 TCGACTAAGAACGTGCCCCAAGAGGGCGGAACAACTTTGGATGACTCTAAATATGTAA 1105
Db 281 SerThrLysAsnValAlaGlnGlnGlyGluLysHisLysAspAspSerLysIleCysLys 300
QY 1106 ATATGTTATTCGAGGAGCGTAACGTTGCTTCTGTCGCGTGGCCACGTGTGCGCTGC 1165

Db 301 IleCysTyrSerGluGluValArgAsnValCysPheValProCysGlyHisValAlaCys 320
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QY 1226 GTGCGCTCTACTTCTCG 1243
Db 341 ValArgLeuTyrPheSer 346

RESULT 2

US-09-201-936-12
; Sequence 12, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Cydia pomonella
US-09-201-936-12

Alignment Scores:
Pred. No.: 1.64e-80
Score: 966.00
Percent Similarity: 72.66%
Best Local Similarity: 59.17%
Query Match: 14.44%
DB: 9
Length: 275
Matches: 171
Conservative: 39
Mismatches: 55
Indels: 24
Gaps: 3

US-10-041-859-1 (1-3773) x US-09-201-936-12 (1-275)

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QY 527 GTGTGCTGTGCTTCTGTAAAGTGAATAATTATGAGGTGGGTGGAAGCGACGATCTGCC 586
Db 41 ValArgCysAlaPheCysLysValGluIleMetArgTrpLysGluGluAspProAla 60
QY 587 GCCGATCATCGAGATGGCGCCCGACGTGCTCCCTTTGACGAAACAATATGCGCAAC 646
Db 61 AlaAspHisLysLysTrpAlaProGlnCysProPheValLys----- 74
QY 647 GCTGGGGGAGAGCGCACCGCTGCTGAGAGACGAATGTGGGGCCAGTGGCCACGAG 706
Db 75 -----GlyIleAspValCysGlySerIleValThrThrAsn 86
QY 707 -----CCTCCCGCATGCCGGCGCCCGGTGACAGCGCGGTACTCC 745


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Db      12  LysLysSerGlyLeuGlnMetAspIleThrLysValAlaSerAsnGlySerSerThr 31
QY      248  TTGGTGAATGTTAAAAAT---CGCGGGATGCAAAAATCGACCTTTCATTTGGTCCGCTC 304
Db      32  LeuThrLeuPheLysSerGlySerLeuGlnAlaLysIleArgPro---LeuAlaProLeu 50
QY      305  ATGTTA-----TCCTCGTGTAGTCTTCAACGACATCCACTCCCGTCACTTCTGCTCG 358
Db      51  MetLeuProThrProSerThrAspSerAsnAlaGlySerProSerLeuSerProSerThr 70
QY      359  -----TCACTGATAAACGGATAATCAGACACATTCACATTCACCTTC 397
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QY      398  CTTCTGATATGCCCGACATGCGTCTGTAAAGAGAAAGCTGTGAAACATTTGATCAGTGG 457
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QY      458  CCGGTACGTTTGTACCGCGGAACAATTGGCCCGCAACGATTCTACTACTCTCGTCCG 517
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QY      518  GCGCAGCAAGTGTGTCTTCTTCTGTAAAGTGAATAATTAGAGTGGTGGTGAAGCGCAC 577
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QY      869  TCGCAGCGAGGGCTAAAGATTGGAAAGCGATGACGTTCCGTGGGAAACAGACGCCAGA 928
Db      250  CysAspGlyGlyLeuLysAspTrpGlnAsnHisAspValProTrpGlnGlnHisAlaArg 269
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Db      310  ThrAlaGlnProSerProProAlaGlnAlaProGlnAsnSerValAspAspSerLysLeu 329
QY      1100  TGTAAATATGTTATTCCGAGGAGCGGTAACGTGTCTTCTGCGCGTGGCGCACGTGGTG 1159
Db      330  CysLysIleCysTyrAlaGlnGlnArgAsnValCysPheValProCysGlnHisValVal 349
QY      1160  GCGTCGCGCAAGTGGCGGTGTGACGAGCAACAAGTGGCGATGTGTGACGAGCGTTTCAAG 1219
Db      350  AlaCysAlaLysCysAlaLeuAlaAlaAspLysCysProMetCysArgArgThrPheGln 369
QY      1220  AATGCGGTGGGCTCTACTTCTCG 1243
Db      370  AsnAlaValArgLeuTyrPheSer 377

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RESULT 2
US-08-511-485-12
; Sequence 12, Application US/08511485
; Patent No. 5919912
;
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 275 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: both
; MOLECULE TYPE: protein
; US-08-511-485-12
;
; Alignment Scores:
; Pred. No.: 2.62e-94 Length: 275
; Score: 966.00 Matches: 171
; Percent Similarity: 72.66% Conservative: 39
; Best Local Similarity: 59.17% Mismatches: 55
; Query Match: 14.44% Indels: 24
; DB: 2 Gaps: 3
;
; US-10-041-859-1 (1-3773) x US-08-511-485-12 (1-275)
;
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QY      467  TTTTTCAGCGCCGGAACAATTGGCCCGCAACGATTTCTACTACCTCGTGGCGCGAGCAA 526
Db      21  PheLeuSerProGlnThrMetAlaLysAsnGlyPheTyrTrpLeuGlyArgSerAspGlu 40
QY      527  GTGTCTGTGCTTCTGTAAAGTGAATAATTAGAGTGGTGGTGAAGCGCGACATCTGGCC 586
Db      41  ValArgCysAlaPheCysLysValGlnIleMetArgTrpLysGlnGlyGlnAspProAla 60
QY      587  GCCGATCATCGAGATGGCGCGCCGAGTGTCCCTTGTACGAAACAATGTATGCCAAC 646
Db      61  AlaAspHisLysLysTrpAlaProGlnCysProPheValLys----- 74
QY      647  GCTGGGAGAGGCGACCGCTGTCTGCTAGACGCAATGTGGCGCGACGTGGCGCGACGAG 706

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XX WPI; 2002-590628/63.
DR N-PSDB; ABQ78228.
XX
PT Novel recombinant polypeptide, inhibitor of apoptosis protein family
PT member BmiAP from silkworm Bombyx mori BmN cells, useful for inhibiting
PT apoptosis and identifying an agent that modulates activity of
PT polypeptide.
XX
PS Claim 39; Page 31; 62pp; English.
XX
CC The present scone represents a polypeptide which is an inhibitor of
CC apoptosis protein (IAP) family member, and designated BmiAP. BmiAP is
CC derived from silkworm Bombyx mori BmN cells. The BmiAP polypeptide
CC contains two baculoviral IAP repeat (BIR) domains, followed by a RING
CC domain. BmiAP polypeptides and polynucleotides are useful for inhibiting
CC apoptosis in insect cells, especially Spodoptera frugiperda or Bombyx
CC mori cells, and mammalian cells, and plant cells. They are also useful
CC for generating a biotic or abiotic insult-resistant plant. BmiAP is also
CC useful for inhibiting caspases

XX Sequence 346 AA;

Alignment Scores:

Pred. No.:	2.71e-182	Length:	346
Score:	1887.00	Matches:	346
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	28.20%	Indels:	0
DB:	5	Gaps:	0

US-10-041-859-1 (1-3773) x ABB78046 (1-346)

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Db 1 MetGluLeuThrIysValAlaIysAsnGlyAlaAlaThrLeuValMetLeuIysAsn 20
QY 266 GCGGGGATGCAAAAATGCGACCTTTTCATTGGTCCGCTCATGTTACTCGTGTGAGTCT 325
Db 21 AlaArgAspAlaIysMetArgProPheIleGlyProLeuMetLeuSerSerCysGluSer 40
QY 326 TCAACGACATCCACACTCCCGTCACCTTCGTCAGCTGATATAACGATATACAGAC 385
Db 41 SerThrThrSerThrLeuProSerProSerSerSerAlaAspIysThrAspAsnHisAsp 60
QY 386 ACATTCAACTTCCTTCCTGATATATGCGCAGATGCGTGTGAAGAGAACGCTGAAACA 445
Db 61 ThrPheAsnHeuLeuProAspMetProAspMetArgArgGluGluIuArgLeuIysThr 80
QY 446 TTTGATCAGTGGCCCGTTACGTTTGTGACGCCGGAACAATTGGCCCCCAACGAGATTCTAC 505
Db 81 PheAspGlnTrpProValThrPheLeuThrProGluInLeuAlaArgAsnGlyPheIyr 100
QY 506 TACCTCGGTCCGGCGGCGAGAGTGTGCTGCTTCTGTAAAGTAAATTAATGAGGTGG 565
Db 101 TyrLeuGlyArgGlyAspGluValCysCysAlaPheCysIysValGluIleMetArgTrp 120
QY 566 GTCGAAGGCGACGATCTTGCGCGCGCATCATCGAGATGGCGCCCAAGTGTCCCTTTGTA 625
Db 121 ValGluGlyAspAspProAlaAlaAspHisArgArgTrpAlaProGlnCysProPheVal 140
QY 626 CGAAAACAAAATGTATGCGCAACGCTGGGGGAGAGCGACCGCTGTGGTAGAGACGAATGT 685
Db 141 ArgIysGlnMetTyrAlaAsnAlaGlyGlyAlaThrAlaValGlyArgAspGluCys 160
QY 686 GGGGCCAGTGGCGCCACGAGCCTCCCGCATGCCCCCGCGCCGTCACGCGCGTACTCC 745
Db 161 GlyAlaSerAlaAlaThrGlnProArgMetProGlyProValHisAlaArgTyrSer 180
QY 746 ACCGAGCGCGCGCGCTCGCCACTTCAAGAGACTGGCCGAGACGTATGCGCAAAACC 805
Db 181 ThrGluAlaAlaArgLeuAlaThrPheIysAspTrpProArgArgMetArgGlnIysPro 200

QY 806 GAGGAATTGGCAGAGCGCGGATTCTTTATACAGCCCAAGGTGACAAAAAGAAATGCTTC 865
Db 201 GluGluLeuAlaGluAlaGlyPhePheTyrThrGlnGlnIysAspIysThrIysCysPhe 220
QY 866 TATTGCGACGGAGGGCTAAAGATTGGGAAAGCGATGACGTTCCGTGGAAACAGACAGCC 925
Db 221 TyrCysAspGlyGlyLeuIysAspTrpGluSerAspAspValProTrpGluGlnHisAla 240
QY 926 AGATGTTGCACCGCTGCGCGCTGACATGCTGGAAGAGACGTGACTACATTACAGAG 985
Db 241 ArgTrpPheAspArgCysAlaTyrValGlnLeuValIysGlyArgAspTyrIleGlnIys 260
QY 986 GTGAAGTCGAGCGCCACTGCGCATATCTGCTAGCGAAGAGAACAGCCCGCACCAATGAT 1045
Db 261 ValIysSerGluAlaThrAlaIleSerAlaSerGluGluGlnAlaAlaThrAsnAsp 280
QY 1046 TCGACTAAGAACGTGCGCCCAAGAGCGGAGAAACATTGGATGACTTAAATATGTAA 1105
Db 281 SerThrIysAsnValAlaGlnGlnIuGlyIuIysHisLeuAspAspSerIysIleCysIys 300
QY 1106 ATAATGTTATTCGAGAGACCGTAACGTGTGCTTCGTCGCGGTGCCGACGTGTGCGCTGC 1165
Db 301 IleCysTyrSerGlnGluArgAsnValCysPheValProCysGlyHisValAlaCys 320
QY 1166 GCCAAGTCGCGCGCTGTGCAGACGACAAGTCCCGCATGTGTGCGACGATTACGAATGCG 1225
Db 321 AlaIysCysAlaLeuSerThrAspIysCysProMetCysArgArgThrPheThrAsnAla 340
QY 1226 GTGCGGCTCTACTTCTCG 1243
Db 341 ValArgLeuIyrPheSer 346

RESULT 2
AAE07881

ID AAE07881 standard; protein; 377 AA.

XX AAE07881;

DT 01-NOV-2001 (first entry)

DE Fall armyworm inhibitor of apoptosis (IAP) protein.

KW Fall armyworm; inhibitor of apoptosis; IAP; transgenic plant;
KW apoptosis inhibitor; therapy; acquired immune deficiency syndrome; AIDS;
KW neurodegenerative disease; Alzheimer's disease; aplastic anaemia;
KW Parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa;
KW myelodysplastic syndrome; toxin-induced liver disease; ischaemic injury;
KW myocardial infarction; stroke; reperfusion injury; cancer; nootropic;
KW autoimmune disorder; lupus erythematosus; multiple sclerosis; vasotropic;
KW insecticide; viral infection; anti-HIV; human immunodeficiency virus;
KW neuroprotective; antinaemic; cardiant; cerebroprotective; vulnerary;
KW cyostatic; immunosuppressive; virucide; antialcoholic.

XX Spodoptera frugiperda.

OS WO200159108-A2.

PN 16-AUG-2001.

PD 07-FEB-2001; 2001WO-US004071.

PF 10-FEB-2000; 2000US-00502528.

PR (REGC) UNIV CALIFORNIA.

PA (MAED/) MAEDA H.

PI Maeda S, Hammock BD, Huang Q, Maeda H;

XX WPI; 2001-514667/56.

DR N-PSDB; AAD14419.

PT Novel nucleic acid construct comprising cDNA encoding inhibitor of
apoptosis proteins, useful for controlling apoptosis in target cells and

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 13, 2005, 01:23:43 ; Search time 15375 Seconds
(without alignments)
11604.815 Million cell updates/sec

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Gapop 10.0 , Gapexc 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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VERSION	AX664311.1	GI:29164241			
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ORGANISM	Bombyx mori				
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AUTHORS		Inhibitor of apoptosis proteins and nucleic acids and methods for			
TITLE		making and using them			
JOURNAL		Patent: WO 02053586-A 1 11-JUL-2002;			
		The Burnham Institute (US)			
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VERSION
AX664311.1 GI:29164241
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1 Huang,Q., Reed,J.C., Devereaux,Q.L. and Maeda,S.D.
Inhibitor of apoptosis proteins and nucleic acids and methods for
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Patent: WO 02053586-A 1 11-JUL-2002;
The Burnham Institute (US)
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